GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 12:00:19 ; Search time 174.34 Seconds
(without alignments)
12.741 Million cell updates/sec

Title: US-09-424-080A-2
Perfect score: 11
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 36232

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
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11: /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
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22: /cgn2_6/ptodata/2/paa/US098_COMB.pep:*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*
24: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	36.4	8	1	PCT-US00-00903-105	Sequence 105, App
2	4	36.4	8	1	PCT-US00-01012-48	Sequence 48, Appl
3	4	36.4	8	1	PCT-US00-01602-4	Sequence 4, Appli
4	4	36.4	8	1	PCT-US00-01602-98	Sequence 98, Appl
5	4	36.4	8	1	PCT-US00-01602-104	Sequence 104, App
6	4	36.4	8	1	PCT-US00-01602-154	Sequence 154, App
7	4	36.4	8	1	PCT-US00-01602-159	Sequence 159, App
8	4	36.4	8	1	PCT-US00-01602-161	Sequence 161, App
9	4	36.4	8	1	PCT-US00-01602-162	Sequence 162, App
10	4	36.4	8	1	PCT-US00-01602-186	Sequence 186, App
11	4	36.4	8	1	PCT-US00-03559-2	Sequence 2, Appli
12	4	36.4	8	1	PCT-US00-03559-10	Sequence 10, Appl
13	4	36.4	8	1	PCT-US00-03559-11	Sequence 11, Appl
14	4	36.4	8	1	PCT-US00-03559-12	Sequence 12, Appl
15	4	36.4	8	1	PCT-US00-03559-16	Sequence 16, Appl
16	4	36.4	8	1	PCT-US00-03559-17	Sequence 17, Appl
17	4	36.4	8	1	PCT-US00-03864-16	Sequence 16, Appl
18	4	36.4	8	1	PCT-US00-04565-2	Sequence 2, Appli
19	4	36.4	8	1	PCT-US00-06043-67	Sequence 67, Appl
20	4	36.4	8	1	PCT-US00-06166-1	Sequence 1, Appli
21	4	36.4	8	1	PCT-US00-06765-85	Sequence 85, Appl
22	4	36.4	8	1	PCT-US00-06765-85	Sequence 85, Appl
23	4	36.4	8	1	PCT-US00-06823-90	Sequence 90, Appl
24	4	36.4	8	1	PCT-US00-06823-121	Sequence 121, App
25	4	36.4	8	1	PCT-US00-06823-122	Sequence 122, App
26	4	36.4	8	1	PCT-US00-06828-93	Sequence 93, Appl
27	4	36.4	8	1	PCT-US00-06830-86	Sequence 86, Appl
28	4	36.4	8	1	PCT-US00-07507-109	Sequence 109, App
29	4	36.4	8	1	PCT-US00-07578B-126	Sequence 126, App
30	4	36.4	8	1	PCT-US00-07579-103	Sequence 103, App
31	4	36.4	8	1	PCT-US00-07686-46	Sequence 46, Appl
32	4	36.4	8	1	PCT-US00-07725-96	Sequence 96, Appl
33	4	36.4	8	1	PCT-US00-08347-3	Sequence 3, Appli
34	4	36.4	8	1	PCT-US00-08561-45	Sequence 45, Appl
35	4	36.4	8	1	PCT-US00-08746-6	Sequence 6, Appli
36	4	36.4	8	1	PCT-US00-08979-261	Sequence 261, App
37	4	36.4	8	1	PCT-US00-09068-83	Sequence 83, Appl
38	4	36.4	8	1	PCT-US00-09069-74	Sequence 74, Appl
39	4	36.4	8	1	PCT-US00-09069-74	Sequence 74, Appl
40	4	36.4	8	1	PCT-US00-09465-7	Sequence 7, Appli
41	4	36.4	8	1	PCT-US00-10344-25	Sequence 25, Appl
42	4	36.4	8	1	PCT-US00-12788-361	Sequence 361, App
43	4	36.4	8	1	PCT-US00-13292-35	Sequence 35, Appl
44	4	36.4	8	1	PCT-US00-14687-6	Sequence 6, Appli
45	4	36.4	8	24	US-60-185-205-142	Sequence 142, App

ALIGNMENTS

RESULT 1
PCT-US00-00903-105
; Sequence 105, Application PC/TUS0000903
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 33 Human Secreted Proteins
; FILE REFERENCE: PZ036.PCT
; CURRENT APPLICATION NUMBER: PCT/US00/00903
; CURRENT FILING DATE: 2000-01-18
; EARLIER APPLICATION NUMBER: 60/116,330
; EARLIER FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-00903-105

Query Match 36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 1 L 1

RESULT 2
PCT-US00-01012-48
; Sequence 48, Application PC/TUS0001012

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; GENERAL INFORMATION:
;  APPLICANT: The Burnham Institute
;  TITLE OF INVENTION: Methods for Inhibiting Tumor Metastasis, and Peptides
;  TITLE OF INVENTION: Useful Therefor
;  FILE REFERENCE: FP-LJ 3865
;  CURRENT APPLICATION NUMBER: PCT/US00/01012
;  CURRENT FILING DATE: 2000-01-14
;  EARLIER APPLICATION NUMBER: 09/232,484
;  EARLIER FILING DATE: 1999-01-05
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: Xaa = any amino acid
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (5)
;   OTHER INFORMATION: Xaa = any amino acid
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (7)..(8)
;   OTHER INFORMATION: Xaa = any amino acid
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Consensus
;   OTHER INFORMATION: Sequence
PCT-US00-01012-48


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       4 L 4


RESULT   3
PCT-US00-01602-4
; Sequence 4, Application PC/TUS0001602
; GENERAL INFORMATION:
;  APPLICANT:  The Burnham Institute
;  TITLE OF INVENTION:  Homing Pro-Apoptotic Conjugates and Methods of Using
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE:  FP-LJ 3866
;  CURRENT APPLICATION NUMBER: PCT/US00/01602
;  CURRENT FILING DATE:  2000-01-21
;  PRIOR APPLICATION NUMBER:  US 09/235,902
;  PRIOR FILING DATE:  1999-01-22
;  NUMBER OF SEQ ID NOS:  235
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
PCT-US00-01602-4


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       2 L 2


RESULT   4
PCT-US00-01602-98
; Sequence 98, Application PC/TUS0001602
; GENERAL INFORMATION:
;  APPLICANT:  The Burnham Institute
;  TITLE OF INVENTION:  Homing Pro-Apoptotic Conjugates and Methods of Using
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE:  FP-LJ 3866
;  CURRENT APPLICATION NUMBER: PCT/US00/01602
;  CURRENT FILING DATE:  2000-01-21
;  PRIOR APPLICATION NUMBER:  US 09/235,902
;  PRIOR FILING DATE:  1999-01-22
;  NUMBER OF SEQ ID NOS:  235
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 98
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
PCT-US00-01602-98


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       6 L 6


RESULT   5
PCT-US00-01602-104
; Sequence 104, Application PC/TUS0001602
; GENERAL INFORMATION:
;  APPLICANT:  The Burnham Institute
;  TITLE OF INVENTION:  Homing Pro-Apoptotic Conjugates and Methods of Using
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE:  FP-LJ 3866
;  CURRENT APPLICATION NUMBER: PCT/US00/01602
;  CURRENT FILING DATE:  2000-01-21
;  PRIOR APPLICATION NUMBER:  US 09/235,902
;  PRIOR FILING DATE:  1999-01-22
;  NUMBER OF SEQ ID NOS:  235
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 104
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
PCT-US00-01602-104


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       4 L 4


RESULT   6
PCT-US00-01602-154
; Sequence 154, Application PC/TUS0001602
; GENERAL INFORMATION:
;  APPLICANT:  The Burnham Institute
```

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;  TITLE OF INVENTION:  Homing Pro-Apoptotic Conjugates and Methods of Using
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE:  FP-LJ 3866
;  CURRENT APPLICATION NUMBER: PCT/US00/01602
;  CURRENT FILING DATE:  2000-01-21
;  PRIOR APPLICATION NUMBER:  US 09/235,902
;  PRIOR FILING DATE:  1999-01-22
;  NUMBER OF SEQ ID NOS:  235
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 154
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
PCT-US00-01602-154


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      5 L 5


RESULT   7
PCT-US00-01602-159
; Sequence 159, Application PC/TUS0001602
; GENERAL INFORMATION:
;  APPLICANT:  The Burnham Institute
;  TITLE OF INVENTION:  Homing Pro-Apoptotic Conjugates and Methods of Using
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE:  FP-LJ 3866
;  CURRENT APPLICATION NUMBER: PCT/US00/01602
;  CURRENT FILING DATE:  2000-01-21
;  PRIOR APPLICATION NUMBER:  US 09/235,902
;  PRIOR FILING DATE:  1999-01-22
;  NUMBER OF SEQ ID NOS:  235
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 159
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
PCT-US00-01602-159


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      4 L 4


RESULT   8
PCT-US00-01602-161
; Sequence 161, Application PC/TUS0001602
; GENERAL INFORMATION:
;  APPLICANT:  The Burnham Institute
;  TITLE OF INVENTION:  Homing Pro-Apoptotic Conjugates and Methods of Using
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE:  FP-LJ 3866
;  CURRENT APPLICATION NUMBER: PCT/US00/01602
;  CURRENT FILING DATE:  2000-01-21
;  PRIOR APPLICATION NUMBER:  US 09/235,902
;  PRIOR FILING DATE:  1999-01-22
;  NUMBER OF SEQ ID NOS:  235
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 161
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
PCT-US00-01602-161


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      3 L 3


RESULT   9
PCT-US00-01602-162
; Sequence 162, Application PC/TUS0001602
; GENERAL INFORMATION:
;  APPLICANT:  The Burnham Institute
;  TITLE OF INVENTION:  Homing Pro-Apoptotic Conjugates and Methods of Using
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE:  FP-LJ 3866
;  CURRENT APPLICATION NUMBER: PCT/US00/01602
;  CURRENT FILING DATE:  2000-01-21
;  PRIOR APPLICATION NUMBER:  US 09/235,902
;  PRIOR FILING DATE:  1999-01-22
;  NUMBER OF SEQ ID NOS:  235
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 162
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
PCT-US00-01602-162


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      3 L 3


RESULT  10
PCT-US00-01602-186
; Sequence 186, Application PC/TUS0001602
; GENERAL INFORMATION:
;  APPLICANT:  The Burnham Institute
;  TITLE OF INVENTION:  Homing Pro-Apoptotic Conjugates and Methods of Using
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE:  FP-LJ 3866
;  CURRENT APPLICATION NUMBER: PCT/US00/01602
;  CURRENT FILING DATE:  2000-01-21
;  PRIOR APPLICATION NUMBER:  US 09/235,902
;  PRIOR FILING DATE:  1999-01-22
;  NUMBER OF SEQ ID NOS:  235
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 186
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

```
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
PCT-US00-01602-186


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      3 L 3


RESULT  11
PCT-US00-03559-2
; Sequence 2, Application PC/TUS0003559A
; GENERAL INFORMATION:
;  APPLICANT:  MUKHERJEE, RAMA
;  APPLICANT:  JAGGI, MANU
;  APPLICANT:  PRASAD, SUDHANAND
;  APPLICANT:  BURMAN, ANAND C
;  APPLICANT:  RAJENDRAN, PRAVEEN
;  APPLICANT:  MATHUR, ARCHANA
;  APPLICANT:  SINGH, ANU T
;  TITLE OF INVENTION:  ANTIANGIOGENIC DRUGS
;  FILE REFERENCE:  09/248,381
;  CURRENT APPLICATION NUMBER: PCT/US00/03559A
;  CURRENT FILING DATE:  2000-02-11
;  PRIOR APPLICATION NUMBER:  09/248,381
;  PRIOR FILING DATE:  1999-02-11
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: This peptide
;   OTHER INFORMATION: was synthetically generated.
PCT-US00-03559-2


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT  12
PCT-US00-03559-10
; Sequence 10, Application PC/TUS0003559A
; GENERAL INFORMATION:
;  APPLICANT:  MUKHERJEE, RAMA
;  APPLICANT:  JAGGI, MANU
;  APPLICANT:  PRASAD, SUDHANAND
;  APPLICANT:  BURMAN, ANAND C
;  APPLICANT:  RAJENDRAN, PRAVEEN
;  APPLICANT:  MATHUR, ARCHANA
;  APPLICANT:  SINGH, ANU T
;  TITLE OF INVENTION:  ANTIANGIOGENIC DRUGS
;  FILE REFERENCE:  09/248,381
;  CURRENT APPLICATION NUMBER: PCT/US00/03559A
;  CURRENT FILING DATE:  2000-02-11
;  PRIOR APPLICATION NUMBER:  09/248,381
;  PRIOR FILING DATE:  1999-02-11
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: This peptide
;   OTHER INFORMATION: was synthetically generated.
;   NAME/KEY: MOD_RES
;   LOCATION: (6)
;   OTHER INFORMATION: /product=D-tyrosine/label=D-Tyr
PCT-US00-03559-10


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT  13
PCT-US00-03559-11
; Sequence 11, Application PC/TUS0003559A
; GENERAL INFORMATION:
;  APPLICANT:  MUKHERJEE, RAMA
;  APPLICANT:  JAGGI, MANU
;  APPLICANT:  PRASAD, SUDHANAND
;  APPLICANT:  BURMAN, ANAND C
;  APPLICANT:  RAJENDRAN, PRAVEEN
;  APPLICANT:  MATHUR, ARCHANA
;  APPLICANT:  SINGH, ANU T
;  TITLE OF INVENTION:  ANTIANGIOGENIC DRUGS
;  FILE REFERENCE:  09/248,381
;  CURRENT APPLICATION NUMBER: PCT/US00/03559A
;  CURRENT FILING DATE:  2000-02-11
;  PRIOR APPLICATION NUMBER:  09/248,381
;  PRIOR FILING DATE:  1999-02-11
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: This peptide
;   OTHER INFORMATION: was synthetically generated.
;   NAME/KEY: MOD_RES
;   LOCATION: (7)
;   OTHER INFORMATION: /product=D-leucine/label=D-Leu
PCT-US00-03559-11


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT  14
PCT-US00-03559-12
; Sequence 12, Application PC/TUS0003559A
; GENERAL INFORMATION:
;  APPLICANT:  MUKHERJEE, RAMA
;  APPLICANT:  JAGGI, MANU
;  APPLICANT:  PRASAD, SUDHANAND
;  APPLICANT:  BURMAN, ANAND C
;  APPLICANT:  RAJENDRAN, PRAVEEN
;  APPLICANT:  MATHUR, ARCHANA
;  APPLICANT:  SINGH, ANU T
;  TITLE OF INVENTION:  ANTIANGIOGENIC DRUGS
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;  FILE REFERENCE:  09/248,381
;  CURRENT APPLICATION NUMBER: PCT/US00/03559A
;  CURRENT FILING DATE:  2000-02-11
;  PRIOR APPLICATION NUMBER:  09/248,381
;  PRIOR FILING DATE:  1999-02-11
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: This peptide
;   OTHER INFORMATION: was synthetically generated.
;   NAME/KEY: MOD_RES
;   LOCATION: (3)
;   OTHER INFORMATION: /product=D-tyrosine/label=D-Tyr
;   NAME/KEY: MOD_RES
;   LOCATION: (7)
;   OTHER INFORMATION: /product=D-leucine/label=D-Leu
PCT-US00-03559-12


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       1 L 1


RESULT  15
PCT-US00-03559-16
; Sequence 16, Application PC/TUS0003559A
; GENERAL INFORMATION:
;  APPLICANT:  MUKHERJEE, RAMA
;  APPLICANT:  JAGGI, MANU
;  APPLICANT:  PRASAD, SUDHANAND
;  APPLICANT:  BURMAN, ANAND C
;  APPLICANT:  RAJENDRAN, PRAVEEN
;  APPLICANT:  MATHUR, ARCHANA
;  APPLICANT:  SINGH, ANU T
;  TITLE OF INVENTION:  ANTIANGIOGENIC DRUGS
;  FILE REFERENCE:  09/248,381
;  CURRENT APPLICATION NUMBER: PCT/US00/03559A
;  CURRENT FILING DATE:  2000-02-11
;  PRIOR APPLICATION NUMBER:  09/248,381
;  PRIOR FILING DATE:  1999-02-11
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: This peptide
;   OTHER INFORMATION: was synthetically generated.
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe;
;   NAME/KEY: MOD_RES
;   LOCATION: (4)
;   OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Aib
PCT-US00-03559-16


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       8 L 8


Search completed: December 13, 2001, 12:00:19
Job time: 282 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 12:00:34 ; Search time 9.12 Seconds
(without alignments)
10.106 Million cell updates/sec

Title: US-09-424-080A-2
Perfect score: 11
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 61579 seqs, 11521160 residues

Total number of hits satisfying chosen parameters: 876

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	36.4	8	1	PCT-US00-03561-28	Sequence 28, Appl
2	4	36.4	8	1	PCT-US01-17103-43	Sequence 43, Appl
3	4	36.4	8	1	PCT-US00-33903-18	Sequence 18, Appl
4	4	36.4	8	1	PCT-US01-27692A-103	Sequence 103, App
5	4	36.4	8	1	PCT-US01-27692A-114	Sequence 114, App
6	4	36.4	8	1	PCT-US01-27692A-241	Sequence 241, App
7	4	36.4	8	1	PCT-US01-28124A-6	Sequence 6, Appli
8	4	36.4	8	1	PCT-US01-28124A-41	Sequence 41, Appl
9	4	36.4	8	1	PCT-US01-28124A-42	Sequence 42, Appl
10	4	36.4	8	1	PCT-US01-28124A-43	Sequence 43, Appl
11	4	36.4	8	1	PCT-US01-28124A-44	Sequence 44, Appl
12	4	36.4	8	1	PCT-US01-28124A-46	Sequence 46, Appl
13	4	36.4	8	1	PCT-US01-28124A-50	Sequence 50, Appl
14	4	36.4	8	1	PCT-US01-28124A-56	Sequence 56, Appl
15	4	36.4	8	1	PCT-US01-28124A-59	Sequence 59, Appl
16	4	36.4	8	1	PCT-US01-28124A-128	Sequence 128, App
17	4	36.4	8	1	PCT-US01-28124A-132	Sequence 132, App
18	4	36.4	8	1	PCT-US01-28124A-133	Sequence 133, App
19	4	36.4	8	1	PCT-US01-28124A-134	Sequence 134, App
20	4	36.4	8	1	PCT-US01-28124A-135	Sequence 135, App
21	4	36.4	8	1	PCT-US01-28124A-262	Sequence 262, App
22	4	36.4	8	4	US-08-453-623-51	Sequence 51, Appl
23	4	36.4	8	4	US-08-816-454B-4	Sequence 4, Appli
24	4	36.4	8	4	US-08-816-454B-103	Sequence 103, App
25	4	36.4	8	4	US-08-816-454B-152	Sequence 152, App
26	4	36.4	8	4	US-08-816-454B-153	Sequence 153, App
27	4	36.4	8	4	US-08-816-454B-155	Sequence 155, App
28	4	36.4	8	4	US-08-816-454B-156	Sequence 156, App
29	4	36.4	8	4	US-08-816-454B-157	Sequence 157, App
30	4	36.4	8	4	US-08-816-454B-158	Sequence 158, App
31	4	36.4	8	4	US-08-816-454B-159	Sequence 159, App
32	4	36.4	8	4	US-08-816-454B-160	Sequence 160, App
33	4	36.4	8	4	US-08-816-454B-170	Sequence 170, App
34	4	36.4	8	4	US-08-816-454B-180	Sequence 180, App
35	4	36.4	8	4	US-08-816-454B-189	Sequence 189, App
36	4	36.4	8	4	US-08-974-685-69	Sequence 69, Appl
37	4	36.4	8	4	US-08-974-685-72	Sequence 72, Appl
38	4	36.4	8	4	US-08-974-685-81	Sequence 81, Appl
39	4	36.4	8	4	US-08-974-685-83	Sequence 83, Appl
40	4	36.4	8	4	US-08-974-685-89	Sequence 89, Appl
41	4	36.4	8	4	US-08-974-685-90	Sequence 90, Appl
42	4	36.4	8	4	US-08-974-685-92	Sequence 92, Appl
43	4	36.4	8	4	US-08-974-685-95	Sequence 95, Appl
44	4	36.4	8	4	US-08-974-685-110	Sequence 110, App
45	4	36.4	8	5	US-09-938-671-161	Sequence 161, App

ALIGNMENTS

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PCT-US00-03561-28
; Sequence 28, Application PC/TUS0003561
; GENERAL INFORMATION:
;  APPLICANT: The General Hospital Corporation
;  TITLE OF INVENTION: Compositions and Methods for Modulating TGF-B Signaling
;  FILE REFERENCE: 11275/86218
;  CURRENT APPLICATION NUMBER: PCT/US00/03561
;  CURRENT FILING DATE:  2000-02-11
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US00-03561-28


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       5 L 5


RESULT   2
PCT-US01-17103-43
; Sequence 43, Application PC/TUS0117103
; GENERAL INFORMATION:
;  APPLICANT: University of Massachusetts
;  TITLE OF INVENTION: INTRAFLAGELLAR TRANSPORT
;  FILE REFERENCE: 07917-145WO1
;  CURRENT APPLICATION NUMBER: PCT/US01/17103
;  CURRENT FILING DATE:  2001-05-24
;  PRIOR APPLICATION NUMBER: US 60/206,923
;  PRIOR FILING DATE: 2000-05-24
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Chlamydomonas reinhardtii
PCT-US01-17103-43


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 L 1
          |
Db      1 L 1


RESULT   3
PCT-US00-33903-18
; Sequence 18, Application PC/TUS0033903
; GENERAL INFORMATION:
;  APPLICANT: JOHNSTON-WILSON, NANCY L.
;  APPLICANT:  SIMS, CHRISTINA D.
;  APPLICANT:  HOFMANN, JEAN-PAUL
;  APPLICANT:  ANDERSON, N. LEIGH
;  APPLICANT:  SHORE, ANDREW D.
;  APPLICANT:  YOLKEN, ROBERT H.
;  APPLICANT:  TORREY, E. FULLER
;  TITLE OF INVENTION: BRAIN PROTEIN MARKERS
;  FILE REFERENCE: 41169
;  CURRENT APPLICATION NUMBER: PCT/US00/33903
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: 60/172,286
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US00-33903-18


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      5 L 5


RESULT   4
PCT-US01-27692A-103
; Sequence 103, Application PC/TUS0127692A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
;  FILE REFERENCE: 005774.P003PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/27692A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 251
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: synthetic construct
PCT-US01-27692A-103


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      3 L 3


RESULT   5
PCT-US01-27692A-114
; Sequence 114, Application PC/TUS0127692A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
;  FILE REFERENCE: 005774.P003PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/27692A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 251
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 114
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: synthetic construct
PCT-US01-27692A-114


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      8 L 8


RESULT   6
PCT-US01-27692A-241
; Sequence 241, Application PC/TUS0127692A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
;  FILE REFERENCE: 005774.P003PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/27692A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 251
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: synthetic construct
PCT-US01-27692A-241


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 L 2


RESULT   7
PCT-US01-28124A-6
; Sequence 6, Application PC/TUS0128124A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Biopanning and Rapid Anaylsis of Selective Interactive Ligands
;  FILE REFERENCE: 005774.P004PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28124A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 289
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
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;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28124A-6


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       7 L 7


RESULT   8
PCT-US01-28124A-41
; Sequence 41, Application PC/TUS0128124A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Biopanning and Rapid Anaylsis of Selective Interactive Ligands (E
;  FILE REFERENCE: 005774.P004PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28124A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 289
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28124A-41


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       6 L 6


RESULT   9
PCT-US01-28124A-42
; Sequence 42, Application PC/TUS0128124A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Biopanning and Rapid Anaylsis of Selective Interactive Ligands (E
;  FILE REFERENCE: 005774.P004PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28124A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 289
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28124A-42


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       2 L 2


RESULT   10
PCT-US01-28124A-43
; Sequence 43, Application PC/TUS0128124A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Biopanning and Rapid Anaylsis of Selective Interactive Ligands
;  FILE REFERENCE: 005774.P004PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28124A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 289
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28124A-43


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       2 L 2


RESULT   11
PCT-US01-28124A-44
; Sequence 44, Application PC/TUS0128124A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Biopanning and Rapid Anaylsis of Selective Interactive Ligands
;  FILE REFERENCE: 005774.P004PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28124A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 289
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28124A-44


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       3 L 3


RESULT   12
PCT-US01-28124A-46
; Sequence 46, Application PC/TUS0128124A
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; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Biopanning and Rapid Anaylsis of Selective Interactive Ligands (E
;  FILE REFERENCE: 005774.P004PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28124A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 289
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28124A-46


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       5 L 5


RESULT  13
PCT-US01-28124A-50
; Sequence 50, Application PC/TUS0128124A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Biopanning and Rapid Anaylsis of Selective Interactive Ligands (E
;  FILE REFERENCE: 005774.P004PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28124A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 289
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28124A-50


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       2 L 2


RESULT  14
PCT-US01-28124A-56
; Sequence 56, Application PC/TUS0128124A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Biopanning and Rapid Anaylsis of Selective Interactive Ligands (E
;  FILE REFERENCE: 005774.P004PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28124A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 289
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28124A-56


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       2 L 2


RESULT  15
PCT-US01-28124A-59
; Sequence 59, Application PC/TUS0128124A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Biopanning and Rapid Anaylsis of Selective Interactive Ligands
;  FILE REFERENCE: 005774.P004PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28124A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 289
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28124A-59


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       7 L 7


Search completed: December 13, 2001, 12:00:34
Job time: 297 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 11:55:37 ; Search time 174.34 Seconds
(without alignments)
12.741 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 36232

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
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7: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep:*
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10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep:*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep:*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep:*
19: /cgn2_6/ptodata/2/paa/US095_COMB.pep:*
20: /cgn2_6/ptodata/2/paa/US096_COMB.pep:*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep:*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep:*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*
24: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	8	18	US-09-424-080-1	Sequence 1, Appli
2	24	57.1	8	10	US-08-669-284-30	Sequence 30, Appl
3	24	57.1	8	10	US-08-669-284A-30	Sequence 30, Appl
4	24	57.1	8	11	US-08-704-499A-15	Sequence 15, Appl
5	24	57.1	8	11	US-08-704-499A-16	Sequence 16, Appl
6	24	57.1	8	16	US-09-232-186-15	Sequence 15, Appl
7	24	57.1	8	16	US-09-232-186-16	Sequence 16, Appl
8	21	50.0	8	3	US-07-722-489-409	Sequence 409, App
9	21	50.0	8	8	US-08-403-590B-659	Sequence 659, App
10	21	50.0	8	8	US-08-444-112-659	Sequence 659, App
11	21	50.0	8	19	US-09-535-529-29	Sequence 29, Appl
12	21	50.0	8	19	US-09-535-529-30	Sequence 30, Appl
13	21	50.0	8	19	US-09-535-529-31	Sequence 31, Appl
14	21	50.0	8	19	US-09-535-529-32	Sequence 32, Appl
15	21	50.0	8	20	US-09-633-364-2287	Sequence 2287, Ap
16	20	47.6	8	1	PCT-US98-22376-438	Sequence 438, App
17	20	47.6	8	7	US-08-369-643-47	Sequence 47, Appl
18	20	47.6	8	12	US-08-845-541B-33	Sequence 33, Appl
19	20	47.6	8	14	US-09-065-028-99	Sequence 99, Appl
20	20	47.6	8	16	US-09-296-622-485	Sequence 485, App
21	20	47.6	8	18	US-09-412-863-1615	Sequence 1615, Ap
22	20	47.6	8	18	US-09-412-863-3123	Sequence 3123, Ap
23	20	47.6	8	18	US-09-412-863-5295	Sequence 5295, Ap
24	20	47.6	8	18	US-09-412-863-7909	Sequence 7909, Ap
25	20	47.6	8	18	US-09-412-863-10223	Sequence 10223, A
26	20	47.6	8	18	US-09-412-863-10233	Sequence 10233, A
27	20	47.6	8	18	US-09-412-863-12092	Sequence 12092, A
28	20	47.6	8	18	US-09-438-673-47	Sequence 47, Appl
29	19	45.2	8	5	US-08-183-392A-33	Sequence 33, Appl
30	19	45.2	8	7	US-08-347-414-11	Sequence 11, Appl
31	19	45.2	8	7	US-08-349-177-73	Sequence 73, Appl
32	19	45.2	8	7	US-08-349-177A-73	Sequence 73, Appl
33	19	45.2	8	7	US-08-369-643-48	Sequence 48, Appl
34	19	45.2	8	10	US-08-630-915-65	Sequence 65, Appl
35	19	45.2	8	10	US-08-630-915A-65	Sequence 65, Appl
36	19	45.2	8	14	US-09-099-932-48	Sequence 48, Appl
37	19	45.2	8	18	US-09-412-863-1088	Sequence 1088, Ap
38	19	45.2	8	18	US-09-412-863-1089	Sequence 1089, Ap
39	19	45.2	8	18	US-09-412-863-1090	Sequence 1090, Ap
40	19	45.2	8	18	US-09-412-863-1091	Sequence 1091, Ap
41	19	45.2	8	18	US-09-412-863-4033	Sequence 4033, Ap
42	19	45.2	8	18	US-09-412-863-4034	Sequence 4034, Ap
43	19	45.2	8	18	US-09-412-863-7252	Sequence 7252, Ap
44	19	45.2	8	18	US-09-412-863-7367	Sequence 7367, Ap
45	19	45.2	8	22	US-09-879-957-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-09-424-080-1
; Sequence 1, Application US/09424080
; GENERAL INFORMATION:
; APPLICANT: ZAVIALOV, Vladimir et al.
; TITLE OF INVENTION: COMPOSITION FOR ENHANCING IMMUNOSUPPERSANTS PHARMACEUTICAL ACT
; FILE REFERENCE: 0933-0149P
; CURRENT APPLICATION NUMBER: US/09/424,080
; CURRENT FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunosupressants cylcoporins, FK506, or rapamycin sequences
; OTHER INFORMATION: derived from various organisms using sequence alignment.
US-09-424-080-1

Query Match 100.0%; Score 42; DB 18; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 1 LTEKKYSP 8

RESULT 2
US-08-669-284-30

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; Sequence 30, Application US/08669284
;  GENERAL INFORMATION:
;     APPLICANT:  Inoue, Makoto
;     APPLICANT:  Kikuchi, Kaoru
;     APPLICANT:  Ishige, Yoko
;     APPLICANT:  Ito, Akira
;     APPLICANT:  Kimura, Toru
;     APPLICANT:  Nakayama, Chikao
;     APPLICANT:  Noguchi, Hiroshi
;     TITLE OF INVENTION:  NOVEL HUMAN CILIARY NEUROTROPHIC FACTORS
;     NUMBER OF SEQUENCES:  35
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;       STREET:  2100 Pennsylvania Avenue, N.W.
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20037
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/669,284
;       FILING DATE:  28-JUN-1996
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP94/02269
;       FILING DATE:  27-DEC-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 06-268281
;       FILING DATE:  05-OCT-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 06-201504
;       FILING DATE:  02-AUG-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 05-350934
;       FILING DATE:  29-DEC-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Nakamura, Dean H.
;       REGISTRATION NUMBER:  33,981
;       REFERENCE/DOCKET NUMBER:  Q-42041
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)293-7060
;       TELEFAX:  (202)293-7860
;   INFORMATION FOR SEQ ID NO:  30:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  4..5
;       OTHER INFORMATION:  /product= "See Table 3"
US-08-669-284-30


  Query Match           57.1%;  Score 24;  DB 10;  Length 8;
  Best Local Similarity   62.5%;  Pred. No. 2.9e+06;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||   |||
Db      1 LTTXXYSP 8


RESULT   3
US-08-669-284A-30
; Sequence 30, Application US/08669284A
;  GENERAL INFORMATION:
;     APPLICANT:  Inoue, Makoto
;     APPLICANT:  Kikuchi, Kaoru
;     APPLICANT:  Ishige, Yoko
;     APPLICANT:  Ito, Akira
;     APPLICANT:  Kimura, Toru
;     APPLICANT:  Nakayama, Chikao
;     APPLICANT:  Noguchi, Hiroshi
;     TITLE OF INVENTION:  NOVEL HUMAN CILIARY NEUROTROPHIC FACTORS
;     NUMBER OF SEQUENCES:  35
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;       STREET:  2100 Pennsylvania Avenue, N.W.
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20037
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/669,284A
;       FILING DATE:  28-JUN-1996
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP94/02269
;       FILING DATE:  27-DEC-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 06-268281
;       FILING DATE:  05-OCT-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 06-201504
;       FILING DATE:  02-AUG-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 05-350934
;       FILING DATE:  29-DEC-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Nakamura, Dean H.
;       REGISTRATION NUMBER:  33,981
;       REFERENCE/DOCKET NUMBER:  Q-42041
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)293-7060
;       TELEFAX:  (202)293-7860
;   INFORMATION FOR SEQ ID NO:  30:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  4..5
;       OTHER INFORMATION:  /product= "See Table 3"
US-08-669-284A-30


  Query Match           57.1%;  Score 24;  DB 10;  Length 8;
  Best Local Similarity   62.5%;  Pred. No. 2.9e+06;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||   |||
Db      1 LTTXXYSP 8


RESULT   4
US-08-704-499A-15
; Sequence 15, Application US/08704499A
;  GENERAL INFORMATION:
;     APPLICANT:  Rath, Matthias
;     TITLE OF INVENTION:  HYDROPHILIC SIGNAL
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; TITLE OF INVENTION: OLIGOPEPTIDES AND METHODS OF THERAPEUTIC USE
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INHOUSE IP MANAGEMENT
; STREET: 280 Colorado Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: MS WORD 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,499A
; FILING DATE: AUGUST 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ALI KAMAREI
; REGISTRATION NUMBER: 37000
; REFERENCE/DOCKET NUMBER: 10262US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-7371
; TELEFAX: 415-322-7389
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-499A-15

Query Match 57.1%; Score 24; DB 11; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TEKKY 6
||| :|
Db 3 TEKRY 7

RESULT 5
US-08-704-499A-16
; Sequence 16, Application US/08704499A
; GENERAL INFORMATION:
; APPLICANT: Rath, Matthias
; TITLE OF INVENTION: HYDROPHILIC SIGNAL
; TITLE OF INVENTION: OLIGOPEPTIDES AND METHODS OF THERAPEUTIC USE
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INHOUSE IP MANAGEMENT
; STREET: 280 Colorado Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: MS WORD 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,499A
; FILING DATE: AUGUST 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ALI KAMAREI
; REGISTRATION NUMBER: 37000
; REFERENCE/DOCKET NUMBER: 10262US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-7371
; TELEFAX: 415-322-7389
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-499A-16

Query Match 57.1%; Score 24; DB 11; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TEKKY 6
||| :|
Db 3 TEKRY 7

RESULT 6
US-09-232-186-15
; Sequence 15, Application US/09232186
; GENERAL INFORMATION:
; APPLICANT: Rath, Matthias
; TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PRTOEIN SIGNAL OLIGOPEPTI
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INHOUSE IP MANAGEMENT
; STREET: 280 Colorado Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: MS WORD 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/232,186
; FILING DATE: JANUARY 13, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ALI KAMAREI
; REGISTRATION NUMBER: 37000
; REFERENCE/DOCKET NUMBER: 10262-1US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-322-7371
; TELEFAX: 650-322-7389
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-232-186-15

Query Match 57.1%; Score 24; DB 16; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TEKKY 6
||| :|
Db 3 TEKRY 7

RESULT 7
US-09-232-186-16
; Sequence 16, Application US/09232186
; GENERAL INFORMATION:
; APPLICANT: Rath, Matthias
; TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PRTOEIN SIGNAL OLIGOPEPTI

```
;    NUMBER OF SEQUENCES:  360
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INHOUSE IP MANAGEMENT
;      STREET:  280 Colorado Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk, 3.50 inch, 1.44MB Storage
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  WINDOWS 95
;      SOFTWARE:  MS WORD 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/232,186
;      FILING DATE:  JANUARY 13, 1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ALI KAMAREI
;      REGISTRATION NUMBER:  37000
;      REFERENCE/DOCKET NUMBER:  10262-1US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-322-7371
;      TELEFAX:  650-322-7389
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-232-186-16


  Query Match             57.1%;  Score 24;  DB 16;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 2.9e+06;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TEKKY 6
          |||:|
Db      3 TEKRY 7


RESULT   8
US-07-722-489-409
; Sequence 409, Application US/07722489
;  GENERAL INFORMATION:
;    APPLICANT:  Chien, David Y.
;    APPLICANT:  Rutter, William J.
;    TITLE OF INVENTION:  NANBV Diagnostics and Vaccines
;    NUMBER OF SEQUENCES:  524
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton Street
;      CITY:  Emeryville
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94608
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/722,489
;      FILING DATE:  19910624
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Blackburn, Robert P.
;      REGISTRATION NUMBER:  30,447
;      REFERENCE/DOCKET NUMBER:  0110.031
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2702
;      TELEFAX:  (510) 655-3542(2)
;  INFORMATION FOR SEQ ID NO:  409:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-722-489-409


  Query Match             50.0%;  Score 21;  DB 3;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+06;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 LTEKKY 6
          |||: |
Db      1 LTERLY 6


RESULT   9
US-08-403-590B-659
; Sequence 659, Application US/08403590B
;  GENERAL INFORMATION:
;    APPLICANT:  Chien, David Y.
;    APPLICANT:  Rutter, William J.
;    TITLE OF INVENTION:  NANBV Diagnostics and Vaccines
;    NUMBER OF SEQUENCES:  777
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton Street
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,590B
;      FILING DATE:  14-MAR-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Harbin, Alisa A.
;      REGISTRATION NUMBER:  33,895
;      REFERENCE/DOCKET NUMBER:  0110.002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (508)359-3876
;      TELEFAX:  (508)359-3885
;  INFORMATION FOR SEQ ID NO:  659:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-403-590B-659


  Query Match             50.0%;  Score 21;  DB 8;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+06;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 LTEKKY 6
          |||: |
Db      1 LTERLY 6


RESULT  10
US-08-444-112-659
; Sequence 659, Application US/08444112
;  GENERAL INFORMATION:
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;    APPLICANT:  Chien, David Y.
;    APPLICANT:  Rutter, William J.
;    TITLE OF INVENTION:  NANBV Diagnostics and Vaccines
;    NUMBER OF SEQUENCES:  777
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton Street
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/444,112
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,590
;      FILING DATE:  14-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Harbin, Alisa A.
;      REGISTRATION NUMBER:  33,895
;      REFERENCE/DOCKET NUMBER:  0110.002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (508)359-3876
;      TELEFAX:  (508)359-3885
;  INFORMATION FOR SEQ ID NO:  659:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-444-112-659


  Query Match             50.0%;  Score 21;  DB 8;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+06;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKY 6
           |||: |
Db       1 LTERLY 6


RESULT  11
US-09-535-529-29
; Sequence 29, Application US/09535529
; GENERAL INFORMATION:
;  APPLICANT:  JUNGBAUER, ALOIS
;  APPLICANT:  JOSIC, DJURO
;  APPLICANT:  NECINA, ROMAN
;  TITLE OF INVENTION:  PEPTIDE HAVING AFFINITY FOR COAGULATION FACTOR VIII
;  FILE REFERENCE:  10496/P65152US0
;  CURRENT APPLICATION NUMBER: US/09/535,529
;  CURRENT FILING DATE:  2000-03-27
;  NUMBER OF SEQ ID NOS:  94
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 29
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-09-535-529-29


  Query Match             50.0%;  Score 21;  DB 19;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 2.9e+06;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KKYSP 8
           |:|:|
Db       4 KEYAP 8


RESULT  12
US-09-535-529-30
; Sequence 30, Application US/09535529
; GENERAL INFORMATION:
;  APPLICANT:  JUNGBAUER, ALOIS
;  APPLICANT:  JOSIC, DJURO
;  APPLICANT:  NECINA, ROMAN
;  TITLE OF INVENTION:  PEPTIDE HAVING AFFINITY FOR COAGULATION FACTOR VIII
;  FILE REFERENCE:  10496/P65152US0
;  CURRENT APPLICATION NUMBER: US/09/535,529
;  CURRENT FILING DATE:  2000-03-27
;  NUMBER OF SEQ ID NOS:  94
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 30
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-09-535-529-30


  Query Match             50.0%;  Score 21;  DB 19;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 2.9e+06;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KKYSP 8
           |:|:|
Db       3 KEYAP 7


RESULT  13
US-09-535-529-31
; Sequence 31, Application US/09535529
; GENERAL INFORMATION:
;  APPLICANT:  JUNGBAUER, ALOIS
;  APPLICANT:  JOSIC, DJURO
;  APPLICANT:  NECINA, ROMAN
;  TITLE OF INVENTION:  PEPTIDE HAVING AFFINITY FOR COAGULATION FACTOR VIII
;  FILE REFERENCE:  10496/P65152US0
;  CURRENT APPLICATION NUMBER: US/09/535,529
;  CURRENT FILING DATE:  2000-03-27
;  NUMBER OF SEQ ID NOS:  94
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-09-535-529-31


  Query Match             50.0%;  Score 21;  DB 19;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 2.9e+06;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KKYSP 8
           |:|:|
Db       2 KEYAP 6


RESULT  14
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US-09-535-529-32
; Sequence 32, Application US/09535529
; GENERAL INFORMATION:
;  APPLICANT:  JUNGBAUER, ALOIS
;  APPLICANT:  JOSIC, DJURO
;  APPLICANT:  NECINA, ROMAN
;  TITLE OF INVENTION:  PEPTIDE HAVING AFFINITY FOR COAGULATION FACTOR VIII
;  FILE REFERENCE:  10496/P65152US0
;  CURRENT APPLICATION NUMBER: US/09/535,529
;  CURRENT FILING DATE:  2000-03-27
;  NUMBER OF SEQ ID NOS:  94
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-09-535-529-32


  Query Match             50.0%;  Score 21;  DB 19;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 2.9e+06;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KKYSP 8
            |:|:|
Db       1 KEYAP 5


RESULT  15
US-09-633-364-2287
; Sequence 2287, Application US/09633364
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Keogh, Elissa
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Inducing Cellular Immune Responses to
;  TITLE OF INVENTION:  Prostate Cancer Antigens Using Peptide and Nucleic Acid
;  TITLE OF INVENTION:  Compositions
;  FILE REFERENCE: 018623-014710US
;  CURRENT APPLICATION NUMBER: US/09/633,364
;  CURRENT FILING DATE:  2000-08-07
;  PRIOR APPLICATION NUMBER: US 60/171,312
;  PRIOR FILING DATE: 1999-12-21
;  NUMBER OF SEQ ID NOS: 6899
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2287
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-633-364-2287


  Query Match             50.0%;  Score 21;  DB 20;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+06;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 EKKYSP 8
            || | |
Db       1 EKFYDP 6


Search completed: December 13, 2001, 12:00:19
Job time: 282 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 11:55:37 ; Search time 9.12 Seconds
(without alignments)
10.106 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 61579 seqs, 11521160 residues

Total number of hits satisfying chosen parameters: 876

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	8	5	US-09-424-080A-1	Sequence 1, Appli
2	18	42.9	8	5	US-09-620-394B-8370	Sequence 8370, Ap
3	18	42.9	8	5	US-09-637-780B-640	Sequence 640, App
4	18	42.9	8	5	US-09-849-092A-2	Sequence 2, Appli
5	17	40.5	8	5	US-09-104-337A-466	Sequence 466, App
6	17	40.5	8	5	US-09-528-200-38	Sequence 38, Appl
7	17	40.5	8	5	US-09-528-200-44	Sequence 44, Appl
8	17	40.5	8	5	US-09-528-200-50	Sequence 50, Appl
9	16	38.1	8	5	US-09-104-337A-423	Sequence 423, App
10	16	38.1	8	5	US-09-763-982-12	Sequence 12, Appl
11	16	38.1	8	5	US-09-620-394B-8589	Sequence 8589, Ap
12	16	38.1	8	5	US-09-485-345-10	Sequence 10, Appl
13	16	38.1	8	5	US-09-637-780B-859	Sequence 859, App
14	15	35.7	8	1	PCT-US01-28124A-134	Sequence 134, App
15	15	35.7	8	5	US-09-622-978-18	Sequence 18, Appl
16	15	35.7	8	5	US-09-104-337A-478	Sequence 478, App
17	15	35.7	8	5	US-09-104-337A-526	Sequence 526, App
18	15	35.7	8	5	US-09-486-625A-24	Sequence 24, Appl
19	15	35.7	8	5	US-09-938-497-6	Sequence 6, Appli
20	15	35.7	8	5	US-09-423-468A-9	Sequence 9, Appli
21	15	35.7	8	5	US-09-897-107-39	Sequence 39, Appl
22	15	35.7	8	5	US-09-897-107-43	Sequence 43, Appl
23	14	33.3	8	5	US-09-973-278-661	Sequence 661, App
24	14	33.3	8	5	US-09-104-337A-363	Sequence 363, App
25	14	33.3	8	5	US-09-104-337A-448	Sequence 448, App
26	14	33.3	8	5	US-09-104-337A-496	Sequence 496, App
27	14	33.3	8	5	US-09-104-337A-504	Sequence 504, App
28	14	33.3	8	5	US-09-295-996A-14	Sequence 14, Appl
29	14	33.3	8	5	US-09-982-172-123	Sequence 123, App
30	14	33.3	8	5	US-09-763-982-8	Sequence 8, Appli
31	14	33.3	8	5	US-09-831-047C-121	Sequence 121, App
32	14	33.3	8	5	US-09-837-138-22	Sequence 22, Appl
33	13	31.0	8	4	US-08-816-454B-114	Sequence 114, App
34	13	31.0	8	5	US-09-966-707-20	Sequence 20, Appl
35	13	31.0	8	5	US-09-856-812-14	Sequence 14, Appl
36	13	31.0	8	5	US-09-852-424-52	Sequence 52, Appl
37	13	31.0	8	5	US-09-705-160-40	Sequence 40, Appl
38	13	31.0	8	5	US-09-324-782-18	Sequence 18, Appl
39	13	31.0	8	5	US-09-620-394B-8419	Sequence 8419, Ap
40	13	31.0	8	5	US-09-574-735C-34	Sequence 34, Appl
41	13	31.0	8	5	US-09-637-780B-689	Sequence 689, App
42	13	31.0	8	5	US-09-169-717E-13	Sequence 13, Appl
43	13	31.0	8	5	US-09-938-406-16	Sequence 16, Appl
44	12	28.6	8	1	PCT-US01-28124A-52	Sequence 52, Appl
45	12	28.6	8	4	US-08-816-454B-173	Sequence 173, App

ALIGNMENTS

RESULT 1
US-09-424-080A-1
; Sequence 1, Application US/09424080A
; GENERAL INFORMATION:
; APPLICANT: ZAVIALOV, Vladimir et al.
; TITLE OF INVENTION: COMPOSITION FOR ENHANCING IMMUNOSUPPRESANTS PHARMACEUTICAL ACT
; FILE REFERENCE: 0933-0149P
; CURRENT APPLICATION NUMBER: US/09/424,080A
; CURRENT FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide corresponding to the high-affinity binding/anti-
; OTHER INFORMATION: lymphoproliferative
; OTHER INFORMATION: site of human IFN-alpha
US-09-424-080A-1

Query Match 100.0%; Score 42; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.4e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 1 LTEKKYSP 8

RESULT 2
US-09-620-394B-8370
; Sequence 8370, Application US/09620394B
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-1067P
; CURRENT APPLICATION NUMBER: US/09/620,394B
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9131
; SEQ ID NO 8370
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus Pattern from various organisms
US-09-620-394B-8370

```
  Query Match             42.9%;  Score 18;  DB 5;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 5.4e+04;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 EKKYS 7
           ||:::|
Db       2 EKRHS 6


RESULT   3
US-09-637-780B-640
; Sequence 640, Application US/09637780B
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Thereby
;  FILE REFERENCE: 2750-1096P
;  CURRENT APPLICATION NUMBER: US/09/637,780B
;  CURRENT FILING DATE:  2000-08-11
;  NUMBER OF SEQ ID NOS: 1401
; SEQ ID NO 640
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Consensus Pattern from various organisms
US-09-637-780B-640


  Query Match             42.9%;  Score 18;  DB 5;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 5.4e+04;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 EKKYS 7
           ||:::|
Db       2 EKRHS 6


RESULT   4
US-09-849-092A-2
; Sequence 2, Application US/09849092A
;   GENERAL INFORMATION:
;        APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna
;        TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH
;                            CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL DEHYDROGEN
;                            ACTIVITY, AND WHICH ASSOCIATES WITH P63, A PORTION OF A
;                            RETINOL BINDING PROTEIN RECEPTOR
;        NUMBER OF SEQUENCES: 41
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Felfe & Lynch
;             STREET: 805 Third Avenue
;             CITY: New York City
;             STATE: New York
;             ZIP: 10022
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Wordperfect
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/849,092A
;             FILING DATE: 04-May-2001
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/729,594
;             FILING DATE: 1998-01-27
;             APPLICATION NUMBER: 08/375,962
;             FILING DATE: 20-January-1995
;             APPLICATION NUMBER: 08/258,418
;             FILING DATE: 10-June-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, Norman D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 5372.3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 688-9200
;             TELEFAX: (212) 838-3884
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 8 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-849-092A-2


  Query Match             42.9%;  Score 18;  DB 5;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 YSP 8
           |||
Db       1 YSP 3


RESULT   5
US-09-104-337A-466
; Sequence 466, Application US/09104337A
;   GENERAL INFORMATION:
;        APPLICANT: Winter, Gregory Paul
;                   Griffiths, Andrew David
;                   Williams, Samuel Cameron
;                   Waterhouse, Peter
;                   Nissim, Ahuva
;                   Johnson, Kevin Stuart
;                   Smith, Andrew John Hammond
;        TITLE OF INVENTION: Methods for producing members of specific
;                            binding pairs
;        NUMBER OF SEQUENCES: 600
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Audrey L. Bartnicki
;             STREET: Marshall, Gerstein & Borun
;                     6300 Sears Tower, 233 South Wacker Drive
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60606-6402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/104,337A
;             FILING DATE: 25-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/350,260
;             FILING DATE: 05-DEC-1994
;             APPLICATION NUMBER: GB 9110549.4
;             FILING DATE: 15-MAY-1991
;             APPLICATION NUMBER: GB 9206318.9
;             FILING DATE: 24-MAR-1992
;             APPLICATION NUMBER: PCT/GB92/00883
;             FILING DATE: 15-MAY-1992
;             APPLICATION NUMBER: PCT/GB93/00605
;             FILING DATE: 24-MAR-1993
;             APPLICATION NUMBER: US 08/150,002
;             FILING DATE: 31-MAR-1994
;             APPLICATION NUMBER: US 08/307,619
;             FILING DATE: 16-SEP-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bartnicki, Audrey L.
```

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;             REGISTRATION NUMBER: 40,499
;             REFERENCE/DOCKET NUMBER: 28111/32372A
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312-474-6300
;   INFORMATION FOR SEQ ID NO: 466:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 8 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 466:
US-09-104-337A-466


  Query Match           40.5%;  Score 17;  DB 5;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 5.4e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KKY 6
          |||
Db      1 KKY 3


RESULT   6
US-09-528-200-38
; Sequence 38, Application US/09528200
; GENERAL INFORMATION:
;  APPLICANT: LICHA, KAI
;  APPLICANT:  BECKER, ANDREAS
;  APPLICANT:  SEMMLER, WOLFHARD
;  APPLICANT:  WEIDENMANN, BERTRAM
;  APPLICANT:  HESSNIUS, CARTSEN
;  APPLICANT:  VOLKMER-ENGERT, RUDOLF
;  APPLICANT:  SCHNEIDER-MERGENER, JENS
;  APPLICANT:  BHARGAVA, SARAH
;  TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
;  TITLE OF INVENTION:  FOR OPTICAL DIAGNOSIS
;  FILE REFERENCE: SCH-1731
;  CURRENT APPLICATION NUMBER: US/09/528,200
;  CURRENT FILING DATE:  2000-03-17
;  PRIOR APPLICATION NUMBER: DE 199 17 713.9
;  PRIOR FILING DATE: 1999-09-04
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-528-200-38


  Query Match           40.5%;  Score 17;  DB 5;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 5.4e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KKY 6
          |||
Db      3 KKY 5


RESULT   7
US-09-528-200-44
; Sequence 44, Application US/09528200
; GENERAL INFORMATION:
;  APPLICANT: LICHA, KAI
;  APPLICANT:  BECKER, ANDREAS
;  APPLICANT:  SEMMLER, WOLFHARD
;  APPLICANT:  WEIDENMANN, BERTRAM
;  APPLICANT:  HESSNIUS, CARTSEN
;  APPLICANT:  VOLKMER-ENGERT, RUDOLF
;  APPLICANT:  SCHNEIDER-MERGENER, JENS
;  APPLICANT:  BHARGAVA, SARAH
;  TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
;  TITLE OF INVENTION:  FOR OPTICAL DIAGNOSIS
;  FILE REFERENCE: SCH-1731
;  CURRENT APPLICATION NUMBER: US/09/528,200
;  CURRENT FILING DATE:  2000-03-17
;  PRIOR APPLICATION NUMBER: DE 199 17 713.9
;  PRIOR FILING DATE: 1999-09-04
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-528-200-44


  Query Match           40.5%;  Score 17;  DB 5;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 5.4e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KKY 6
          |||
Db      4 KKY 6


RESULT   8
US-09-528-200-50
; Sequence 50, Application US/09528200
; GENERAL INFORMATION:
;  APPLICANT: LICHA, KAI
;  APPLICANT:  BECKER, ANDREAS
;  APPLICANT:  SEMMLER, WOLFHARD
;  APPLICANT:  WEIDENMANN, BERTRAM
;  APPLICANT:  HESSNIUS, CARTSEN
;  APPLICANT:  VOLKMER-ENGERT, RUDOLF
;  APPLICANT:  SCHNEIDER-MERGENER, JENS
;  APPLICANT:  BHARGAVA, SARAH
;  TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
;  TITLE OF INVENTION:  FOR OPTICAL DIAGNOSIS
;  FILE REFERENCE: SCH-1731
;  CURRENT APPLICATION NUMBER: US/09/528,200
;  CURRENT FILING DATE:  2000-03-17
;  PRIOR APPLICATION NUMBER: DE 199 17 713.9
;  PRIOR FILING DATE: 1999-09-04
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-528-200-50


  Query Match           40.5%;  Score 17;  DB 5;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 5.4e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 KKY 6
          |||
Db      5 KKY 7


RESULT   9
US-09-104-337A-423
; Sequence 423, Application US/09104337A
;   GENERAL INFORMATION:
;       APPLICANT: Winter, Gregory Paul
;                  Griffiths, Andrew David
;                  Williams, Samuel Cameron
;                  Waterhouse, Peter
;                  Nissim, Ahuva
;                  Johnson, Kevin Stuart
;                  Smith, Andrew John Hammond
;       TITLE OF INVENTION: Methods for producing members of specific
```

```
;                          binding pairs
;       NUMBER OF SEQUENCES: 600
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Audrey L. Bartnicki
;            STREET: Marshall, Gerstein & Borun
;                    6300 Sears Tower, 233 South Wacker Drive
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60606-6402
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/104,337A
;            FILING DATE: 25-Jun-1998
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/350,260
;            FILING DATE: 05-DEC-1994
;            APPLICATION NUMBER: GB 9110549.4
;            FILING DATE: 15-MAY-1991
;            APPLICATION NUMBER: GB 9206318.9
;            FILING DATE: 24-MAR-1992
;            APPLICATION NUMBER: PCT/GB92/00883
;            FILING DATE: 15-MAY-1992
;            APPLICATION NUMBER: PCT/GB93/00605
;            FILING DATE: 24-MAR-1993
;            APPLICATION NUMBER: US 08/150,002
;            FILING DATE: 31-MAR-1994
;            APPLICATION NUMBER: US 08/307,619
;            FILING DATE: 16-SEP-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bartnicki, Audrey L.
;            REGISTRATION NUMBER: 40,499
;            REFERENCE/DOCKET NUMBER: 28111/32372A
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312-474-6300
;   INFORMATION FOR SEQ ID NO: 423:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 8 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 423:
US-09-104-337A-423


  Query Match             38.1%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 5.4e+04;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 EKKY 6
           ::||
Db       2 QRKY 5


RESULT  10
US-09-763-982-12
; Sequence 12, Application US/09763982
; GENERAL INFORMATION:
;  APPLICANT: Diamond, Scott L
;  APPLICANT:  THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
;  TITLE OF INVENTION: PEPTIDE SCAFFOLDS FOR TRANSFER OF MOLECULES INTO
;  TITLE OF INVENTION:  EUKARYOTIC CELLS
;  FILE REFERENCE: PENN-0698
;  CURRENT APPLICATION NUMBER: US/09/763,982
;  CURRENT FILING DATE:  2001-09-21
;  PRIOR APPLICATION NUMBER: 60/098,791
;  PRIOR FILING DATE: 1998-09-01
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-763-982-12


  Query Match             38.1%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 5.4e+04;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TEKK 5
           |:||
Db       3 TKKK 6


RESULT  11
US-09-620-394B-8589
; Sequence 8589, Application US/09620394B
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
;  TITLE OF INVENTION:  Thereby
;  FILE REFERENCE: 2750-1067P
;  CURRENT APPLICATION NUMBER: US/09/620,394B
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 9131
; SEQ ID NO 8589
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Consensus Pattern from various organisms
US-09-620-394B-8589


  Query Match             38.1%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 5.4e+04;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TEKK 5
             ||:|
Db       3 TEQK 6


RESULT  12
US-09-485-345-10
; Sequence 10, Application US/09485345
; GENERAL INFORMATION:
;  APPLICANT: Acres, Bruce
;  TITLE OF INVENTION: TGFBeta RII Receptor Nucleic Sequence, Coded Peptide, and Uses
;  FILE REFERENCE: 032847-003
;  CURRENT APPLICATION NUMBER: US/09/485,345
;  CURRENT FILING DATE:  2000-06-28
;  PRIOR APPLICATION NUMBER: PCT/FR99/01354
;  PRIOR FILING DATE: 1999-06-08
;  PRIOR APPLICATION NUMBER: FR 98/07322
;  PRIOR FILING DATE: 1998-06-08
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide capable of binding to at least one MHC I
;   OTHER INFORMATION: glycoprotein.
US-09-485-345-10
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  Query Match             38.1%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 5.4e+04;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKK 5
           : |||
Db       2 MKEKK 6


RESULT  13
US-09-637-780B-859
; Sequence 859, Application US/09637780B
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Thereby
;  FILE REFERENCE: 2750-1096P
;  CURRENT APPLICATION NUMBER: US/09/637,780B
;  CURRENT FILING DATE:  2000-08-11
;  NUMBER OF SEQ ID NOS: 1401
; SEQ ID NO 859
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Consensus Pattern from various organisms
US-09-637-780B-859


  Query Match             38.1%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 5.4e+04;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TEKK 5
           ||:|
Db       3 TEQK 6


RESULT  14
PCT-US01-28124A-134
; Sequence 134, Application PC/TUS0128124A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Biopanning and Rapid Anaylsis of Selective Interactive Ligands (B
;  FILE REFERENCE: 005774.P004PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28124A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 289
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28124A-134


  Query Match             35.7%;  Score 15;  DB 1;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 5.4e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 YSP 8
           |:|
Db       4 YNP 6


RESULT  15
US-09-622-978-18
; Sequence 18, Application US/09622978
; GENERAL INFORMATION:
;  APPLICANT: Hull, Roger
;  APPLICANT:  Harper, Glyn
;  TITLE OF INVENTION: Banana streak virus promoter and detection
;  FILE REFERENCE: 620-106
;  CURRENT APPLICATION NUMBER: US/09/622,978
;  CURRENT FILING DATE:  2000-08-25
;  PRIOR APPLICATION NUMBER: PCT/GB99/00599
;  PRIOR FILING DATE: 1999-02-26
;  PRIOR APPLICATION NUMBER: GB 9804293.0
;  PRIOR FILING DATE: 1998-02-27
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Musa acuminata
US-09-622-978-18


  Query Match             35.7%;  Score 15;  DB 5;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 5.4e+04;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 YSP 8
           |:|
Db       4 YNP 6


Search completed: December 13, 2001, 12:00:34
Job time: 297 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:49:31 ; Search time 181.51 Seconds
(without alignments)
12.238 Million cell updates/sec

Title: US-09-424-080A-2
Perfect score: 11
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
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22: /cgn2_6/ptodata/2/paa/US098_COMB.pep:*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*
24: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	36.4	2	1	PCT-US00-06014-91	Sequence 91, Appl
2	4	36.4	2	1	PCT-US00-29363-207	Sequence 207, App
3	4	36.4	2	1	PCT-US00-30040A-163	Sequence 163, App
4	4	36.4	2	1	PCT-US00-30040A-172	Sequence 172, App
5	4	36.4	2	1	PCT-US00-30045-154	Sequence 154, App
6	4	36.4	2	1	PCT-US00-30629-109	Sequence 109, App
7	4	36.4	2	1	PCT-US00-30629-160	Sequence 160, App
8	4	36.4	2	1	PCT-US00-30653-208	Sequence 208, App
9	4	36.4	2	1	PCT-US01-01786A-159	Sequence 159, App
10	4	36.4	2	1	PCT-US01-11988-168	Sequence 168, App
11	4	36.4	2	1	PCT-US01-11988-476	Sequence 476, App
12	4	36.4	2	1	PCT-US01-11988-494	Sequence 494, App
13	4	36.4	2	1	PCT-US01-11988-665	Sequence 665, App
14	4	36.4	2	1	PCT-US01-11988-1055	Sequence 1055, Ap
15	4	36.4	2	1	PCT-US01-11988-1071	Sequence 1071, Ap
16	4	36.4	2	1	PCT-US01-11988-1072	Sequence 1072, Ap
17	4	36.4	2	1	PCT-US98-03908-53	Sequence 53, Appl
18	4	36.4	2	1	PCT-US98-03908-156	Sequence 156, App
19	4	36.4	2	1	PCT-US99-05496-4	Sequence 4, Appli
20	4	36.4	2	6	US-08-222-626A-113	Sequence 113, App
21	4	36.4	2	8	US-08-452-234A-19	Sequence 19, Appl
22	4	36.4	2	8	US-08-452-454A-19	Sequence 19, Appl
23	4	36.4	2	10	US-08-601-197B-13	Sequence 13, Appl
24	4	36.4	2	10	US-08-633-879B-53	Sequence 53, Appl
25	4	36.4	2	10	US-08-633-879B-79	Sequence 79, Appl
26	4	36.4	2	10	US-08-633-879B-107	Sequence 107, App
27	4	36.4	2	11	US-08-783-798-53	Sequence 53, Appl
28	4	36.4	2	11	US-08-783-798-79	Sequence 79, Appl
29	4	36.4	2	11	US-08-783-798-107	Sequence 107, App
30	4	36.4	2	12	US-08-850-127-53	Sequence 53, Appl
31	4	36.4	2	12	US-08-850-127-156	Sequence 156, App
32	4	36.4	2	15	US-09-110-822-16	Sequence 16, Appl
33	4	36.4	2	15	US-09-149-476-546	Sequence 546, App
34	4	36.4	2	16	US-09-226-402B-35	Sequence 35, Appl
35	4	36.4	2	20	US-09-657-276-738	Sequence 738, App
36	4	36.4	2	20	US-09-657-276-916	Sequence 916, App
37	4	36.4	2	20	US-09-657-276-925	Sequence 925, App
38	4	36.4	2	22	US-09-809-391-546	Sequence 546, App
39	4	36.4	2	22	US-09-833-245-168	Sequence 168, App
40	4	36.4	2	22	US-09-833-245-476	Sequence 476, App
41	4	36.4	2	22	US-09-833-245-494	Sequence 494, App
42	4	36.4	2	22	US-09-833-245-665	Sequence 665, App
43	4	36.4	2	22	US-09-833-245-1055	Sequence 1055, Ap
44	4	36.4	2	22	US-09-833-245-1071	Sequence 1071, Ap
45	4	36.4	2	24	US-60-173-464-9894	Sequence 9894, Ap

ALIGNMENTS

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RESULT 1
PCT-US00-06014-91
; Sequence 91, Application PC/TUS0006014
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: 47 Human Secreted Proteins
;  FILE REFERENCE: PS507PCT
;  CURRENT APPLICATION NUMBER: PCT/US00/06014
;  CURRENT FILING DATE: 2000-03-09
;  EARLIER APPLICATION NUMBER: 60/124,095
;  EARLIER FILING DATE: 1999-03-12
;  EARLIER APPLICATION NUMBER: 60/138,598
;  EARLIER FILING DATE: 0999-06-11
;  EARLIER APPLICATION NUMBER: 60/168,665
;  EARLIER FILING DATE: 1999-12-03
;  NUMBER OF SEQ ID NOS: 148
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
;  LENGTH: 2
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: SITE
;  LOCATION: (2)
;  OTHER INFORMATION: Xaa equals stop translation
PCT-US00-06014-91


  Query Match           36.4%;  Score 4;  DB 1;  Length 2;
  Best Local Similarity  100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 L 1
          |
Db      1 L 1


RESULT   2
PCT-US00-29363-207
; Sequence 207, Application PC/TUS0029363
; GENERAL INFORMATION:
;  APPLICANT:  Human Genome Sciences, Inc.
;  TITLE OF INVENTION:  32 Human Secreted Proteins
;  FILE REFERENCE:  PS701PCT
;  CURRENT APPLICATION NUMBER: PCT/US00/29363
;  CURRENT FILING DATE:  2000-10-25
;  PRIOR APPLICATION NUMBER:  60/162,239
;  PRIOR FILING DATE:  1999-10-29
;  PRIOR APPLICATION NUMBER:  60/215,139
;  PRIOR FILING DATE:  2000-06-30
;  NUMBER OF SEQ ID NOS:  228
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 207
;   LENGTH: 2
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US00-29363-207


  Query Match             36.4%;  Score 4;  DB 1;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT   3
PCT-US00-30040A-163
; Sequence 163, Application PC/TUS0030040A
; GENERAL INFORMATION:
;  APPLICANT:  Human Genome Sciences, Inc.
;  TITLE OF INVENTION:  24 Human Secreted Proteins
;  FILE REFERENCE:  PS706PCT
;  CURRENT APPLICATION NUMBER: PCT/US00/30040A
;  CURRENT FILING DATE:  2000-11-01
;  PRIOR APPLICATION NUMBER:  60/163,580
;  PRIOR FILING DATE:  1999-11-05
;  PRIOR APPLICATION NUMBER:  60/215,130
;  PRIOR FILING DATE:  2000-06-30
;  NUMBER OF SEQ ID NOS:  205
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 163
;   LENGTH: 2
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US00-30040A-163


  Query Match             36.4%;  Score 4;  DB 1;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT   4
PCT-US00-30040A-172
; Sequence 172, Application PC/TUS0030040A
; GENERAL INFORMATION:
;  APPLICANT:  Human Genome Sciences, Inc.
;  TITLE OF INVENTION:  24 Human Secreted Proteins
;  FILE REFERENCE:  PS706PCT
;  CURRENT APPLICATION NUMBER: PCT/US00/30040A
;  CURRENT FILING DATE:  2000-11-01
;  PRIOR APPLICATION NUMBER:  60/163,580
;  PRIOR FILING DATE:  1999-11-05
;  PRIOR APPLICATION NUMBER:  60/215,130
;  PRIOR FILING DATE:  2000-06-30
;  NUMBER OF SEQ ID NOS:  205
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 172
;   LENGTH: 2
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US00-30040A-172


  Query Match             36.4%;  Score 4;  DB 1;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 L 2


RESULT   5
PCT-US00-30045-154
; Sequence 154, Application PC/TUS0030045
; GENERAL INFORMATION:
;  APPLICANT:  Human Genome Sciences, Inc.
;  TITLE OF INVENTION:  28 Human Secreted Proteins
;  FILE REFERENCE:  PS708PCT
;  CURRENT APPLICATION NUMBER: PCT/US00/30045
;  CURRENT FILING DATE:  2000-11-01
;  PRIOR APPLICATION NUMBER:  60/163,581
;  PRIOR FILING DATE:  1999-11-05
;  PRIOR APPLICATION NUMBER:  60/215,133
;  PRIOR FILING DATE:  2000-06-30
;  NUMBER OF SEQ ID NOS:  201
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 154
;   LENGTH: 2
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US00-30045-154


  Query Match             36.4%;  Score 4;  DB 1;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT   6
PCT-US00-30629-109
; Sequence 109, Application PC/TUS0030629
; GENERAL INFORMATION:
;  APPLICANT:  Human Genome Sciences, Inc.
;  TITLE OF INVENTION:  24 Human Secreted Proteins
;  FILE REFERENCE:  PS714PCT
;  CURRENT APPLICATION NUMBER: PCT/US00/30629
;  CURRENT FILING DATE:  2000-11-08
;  PRIOR APPLICATION NUMBER:  60/164,825
;  PRIOR FILING DATE:  1999-11-12
;  PRIOR APPLICATION NUMBER:  60/222,904
;  PRIOR FILING DATE:  2000-08-03
;  NUMBER OF SEQ ID NOS:  189
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 109
;   LENGTH: 2
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;  TYPE: PRT
;  ORGANISM: Homo sapiens
PCT-US00-30629-109


  Query Match           36.4%;  Score 4;  DB 1;  Length 2;
  Best Local Similarity  100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT  7
PCT-US00-30629-160
; Sequence 160, Application PC/TUS0030629
; GENERAL INFORMATION:
;  APPLICANT:  Human Genome Sciences, Inc.
;  TITLE OF INVENTION:  24 Human Secreted Proteins
;  FILE REFERENCE:  PS714PCT
;  CURRENT APPLICATION NUMBER: PCT/US00/30629
;  CURRENT FILING DATE:  2000-11-08
;  PRIOR APPLICATION NUMBER:  60/164,825
;  PRIOR FILING DATE:  1999-11-12
;  PRIOR APPLICATION NUMBER:  60/222,904
;  PRIOR FILING DATE:  2000-08-03
;  NUMBER OF SEQ ID NOS:  189
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 160
;   LENGTH: 2
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US00-30629-160


  Query Match           36.4%;  Score 4;  DB 1;  Length 2;
  Best Local Similarity  100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT  8
PCT-US00-30653-208
; Sequence 208, Application PC/TUS0030653
; GENERAL INFORMATION:
;  APPLICANT:  Human Genome Sciences, Inc.
;  TITLE OF INVENTION:  35 Human Secreted Proteins
;  FILE REFERENCE:  PS713PCT
;  CURRENT APPLICATION NUMBER: PCT/US00/30653
;  CURRENT FILING DATE:  2000-11-08
;  PRIOR APPLICATION NUMBER:  60/164,735
;  PRIOR FILING DATE:  1999-11-12
;  PRIOR APPLICATION NUMBER:  60/221,193
;  PRIOR FILING DATE:  2000-07-27
;  NUMBER OF SEQ ID NOS:  289
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 208
;   LENGTH: 2
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US00-30653-208


  Query Match           36.4%;  Score 4;  DB 1;  Length 2;
  Best Local Similarity  100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 L 2


RESULT  9
PCT-US01-01786A-159
; Sequence 159, Application PC/TUS0101786A
; GENERAL INFORMATION:
;  APPLICANT: SMITHKLINE BEECHAM CORPORATION
;  APPLICANT:  SMITHKLINE BEECHAM p.l.c.
;  TITLE OF INVENTION: METHODS AND REAGENTS FOR PERFORMING
;  TITLE OF INVENTION:  ANTIMICROBIAL COMPOUND SCREENING
;  FILE REFERENCE: GM50067
;  CURRENT APPLICATION NUMBER: PCT/US01/01786A
;  CURRENT FILING DATE:  2001-01-17
;  PRIOR APPLICATION NUMBER: 60/176,870
;  PRIOR FILING DATE: 2000-01-18
;  NUMBER OF SEQ ID NOS: 403
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 159
;   LENGTH: 2
;   TYPE: PRT
;   ORGANISM: Escherichia coli
PCT-US01-01786A-159


  Query Match           36.4%;  Score 4;  DB 1;  Length 2;
  Best Local Similarity  100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT  10
PCT-US01-11988-168
; Sequence 168, Application PC/TUS0111988
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF546PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/11988
;  CURRENT FILING DATE:  2001-01-12
;  PRIOR APPLICATION NUMBER: 60/229, 358
;  PRIOR FILING DATE: 2000-04-12
;  PRIOR APPLICATION NUMBER: 60/256, 931
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/199, 384
;  PRIOR FILING DATE: 2000-04-25
;  NUMBER OF SEQ ID NOS: 2267
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 168
;   LENGTH: 2
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US01-11988-168


  Query Match           36.4%;  Score 4;  DB 1;  Length 2;
  Best Local Similarity  100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT  11
PCT-US01-11988-476
; Sequence 476, Application PC/TUS0111988
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
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;  FILE REFERENCE: PF546PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/11988
;  CURRENT FILING DATE:  2001-01-12
;  PRIOR APPLICATION NUMBER: 60/229, 358
;  PRIOR FILING DATE: 2000-04-12
;  PRIOR APPLICATION NUMBER: 60/256, 931
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/199, 384
;  PRIOR FILING DATE: 2000-04-25
;  NUMBER OF SEQ ID NOS: 2267
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 476
;   LENGTH: 2
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US01-11988-476


  Query Match             36.4%;  Score 4;  DB 1;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT  12
PCT-US01-11988-494
; Sequence 494, Application PC/TUS0111988
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF546PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/11988
;  CURRENT FILING DATE:  2001-01-12
;  PRIOR APPLICATION NUMBER: 60/229, 358
;  PRIOR FILING DATE: 2000-04-12
;  PRIOR APPLICATION NUMBER: 60/256, 931
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/199, 384
;  PRIOR FILING DATE: 2000-04-25
;  NUMBER OF SEQ ID NOS: 2267
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 494
;   LENGTH: 2
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US01-11988-494


  Query Match             36.4%;  Score 4;  DB 1;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 L 2


RESULT  13
PCT-US01-11988-665
; Sequence 665, Application PC/TUS0111988
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF546PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/11988
;  CURRENT FILING DATE:  2001-01-12
;  PRIOR APPLICATION NUMBER: 60/229, 358
;  PRIOR FILING DATE: 2000-04-12
;  PRIOR APPLICATION NUMBER: 60/256, 931
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/199, 384
;  PRIOR FILING DATE: 2000-04-25
;  NUMBER OF SEQ ID NOS: 2267
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 665
;   LENGTH: 2
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US01-11988-665


  Query Match             36.4%;  Score 4;  DB 1;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT  14
PCT-US01-11988-1055
; Sequence 1055, Application PC/TUS0111988
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF546PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/11988
;  CURRENT FILING DATE:  2001-01-12
;  PRIOR APPLICATION NUMBER: 60/229, 358
;  PRIOR FILING DATE: 2000-04-12
;  PRIOR APPLICATION NUMBER: 60/256, 931
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/199, 384
;  PRIOR FILING DATE: 2000-04-25
;  NUMBER OF SEQ ID NOS: 2267
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1055
;   LENGTH: 2
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US01-11988-1055


  Query Match             36.4%;  Score 4;  DB 1;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+06;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 L 2


RESULT  15
PCT-US01-11988-1071
; Sequence 1071, Application PC/TUS0111988
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Albumin Fusion Proteins
;  FILE REFERENCE: PF546PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/11988
;  CURRENT FILING DATE:  2001-01-12
;  PRIOR APPLICATION NUMBER: 60/229, 358
;  PRIOR FILING DATE: 2000-04-12
;  PRIOR APPLICATION NUMBER: 60/256, 931
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/199, 384
;  PRIOR FILING DATE: 2000-04-25
;  NUMBER OF SEQ ID NOS: 2267
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1071
;   LENGTH: 2
;   TYPE: PRT
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; ORGANISM: Homo sapiens
PCT-US01-11988-1071

Query Match 36.4%; Score 4; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 1 L 1

Search completed: December 13, 2001, 10:49:32
Job time: 292 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:49:47 ; Search time 9.21 Seconds
(without alignments)
10.008 Million cell updates/sec

Title: US-09-424-080A-2
Perfect score: 11
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 61579 seqs, 11521160 residues

Total number of hits satisfying chosen parameters: 61579

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	36.4	2	5	US-09-982-172-96	Sequence 96, Appl
2	4	36.4	2	5	US-09-982-172-153	Sequence 153, App
3	4	36.4	2	5	US-09-720-934-101	Sequence 101, App
4	4	36.4	3	1	PCT-US01-27692A-138	Sequence 138, App
5	4	36.4	3	1	PCT-US01-27692A-142	Sequence 142, App
6	4	36.4	3	1	PCT-US01-27692A-161	Sequence 161, App
7	4	36.4	3	1	PCT-US01-27692A-179	Sequence 179, App
8	4	36.4	3	1	PCT-US01-27692A-181	Sequence 181, App
9	4	36.4	3	1	PCT-US01-28044A-8	Sequence 8, Appli
10	4	36.4	3	1	PCT-US01-28044A-9	Sequence 9, Appli
11	4	36.4	3	1	PCT-US01-28044A-10	Sequence 10, Appl
12	4	36.4	3	1	PCT-US01-28044A-15	Sequence 15, Appl
13	4	36.4	3	1	PCT-US01-28044A-21	Sequence 21, Appl
14	4	36.4	3	1	PCT-US01-28044A-130	Sequence 130, App
15	4	36.4	3	1	PCT-US01-28044A-306	Sequence 306, App
16	4	36.4	3	1	PCT-US01-28044A-307	Sequence 307, App
17	4	36.4	3	1	PCT-US01-28044A-309	Sequence 309, App
18	4	36.4	3	1	PCT-US01-28044A-314	Sequence 314, App
19	4	36.4	3	1	PCT-US01-28044A-323	Sequence 323, App
20	4	36.4	3	1	PCT-US01-28044A-345	Sequence 345, App
21	4	36.4	3	1	PCT-US01-28044A-355	Sequence 355, App
22	4	36.4	3	1	PCT-US01-28044A-361	Sequence 361, App
23	4	36.4	3	1	PCT-US01-28044A-363	Sequence 363, App
24	4	36.4	3	1	PCT-US01-28044A-367	Sequence 367, App
25	4	36.4	3	1	PCT-US01-28044A-377	Sequence 377, App
26	4	36.4	3	1	PCT-US01-28044A-380	Sequence 380, App
27	4	36.4	3	1	PCT-US01-28044A-397	Sequence 397, App
28	4	36.4	3	1	PCT-US01-28044A-405	Sequence 405, App
29	4	36.4	3	1	PCT-US01-28044A-406	Sequence 406, App
30	4	36.4	3	1	PCT-US01-28044A-407	Sequence 407, App
31	4	36.4	3	1	PCT-US01-28044A-408	Sequence 408, App
32	4	36.4	3	1	PCT-US01-28044A-409	Sequence 409, App
33	4	36.4	3	1	PCT-US01-28044A-418	Sequence 418, App
34	4	36.4	3	1	PCT-US01-28044A-421	Sequence 421, App
35	4	36.4	3	1	PCT-US01-28044A-423	Sequence 423, App
36	4	36.4	3	5	US-09-967-772-12	Sequence 12, Appl
37	4	36.4	3	5	US-09-982-172-48	Sequence 48, Appl
38	4	36.4	3	5	US-09-982-172-54	Sequence 54, Appl
39	4	36.4	3	5	US-09-720-934-33	Sequence 33, Appl
40	4	36.4	3	5	US-09-720-934-65	Sequence 65, Appl
41	4	36.4	3	5	US-09-720-934-99	Sequence 99, Appl
42	4	36.4	3	5	US-09-922-261-7	Sequence 7, Appli
43	4	36.4	3	5	US-09-922-261-310	Sequence 310, App
44	4	36.4	3	5	US-09-922-261-385	Sequence 385, App
45	4	36.4	4	5	US-09-721-477-71	Sequence 71, Appl

ALIGNMENTS

```
RESULT   1
US-09-982-172-96
; Sequence 96, Application US/09982172
; GENERAL INFORMATION:
;  APPLICANT: Emil Israel Katz
;  TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBO
;  TITLE OF INVENTION:  DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENE
;  TITLE OF INVENTION:  UTILIZING EACH
;  FILE REFERENCE: 01/22283
;  CURRENT APPLICATION NUMBER: US/09/982,172
;  CURRENT FILING DATE:  2001-10-19
;  NUMBER OF SEQ ID NOS: 253
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
;   LENGTH: 2
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-96


  Query Match             36.4%;  Score 4;  DB 5;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       1 L 1


RESULT   2
US-09-982-172-153
; Sequence 153, Application US/09982172
; GENERAL INFORMATION:
;  APPLICANT: Emil Israel Katz
;  TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBO
;  TITLE OF INVENTION:  DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENE
;  TITLE OF INVENTION:  UTILIZING EACH
;  FILE REFERENCE: 01/22283
;  CURRENT APPLICATION NUMBER: US/09/982,172
;  CURRENT FILING DATE:  2001-10-19
;  NUMBER OF SEQ ID NOS: 253
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 153
;   LENGTH: 2
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Computer generated synthetic peptide
```

US-09-982-172-153

Query Match 36.4%; Score 4; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 1 L 1

RESULT 3
US-09-720-934-101
; Sequence 101, Application US/09720934
; GENERAL INFORMATION:
; APPLICANT: Korenberg, Julie R
; APPLICANT: Chen, Xiao-Ning
; TITLE OF INVENTION: ISOLATED SH3 GENES ASSOCIATED WITH MYELOPROLIFERATIVE
; TITLE OF INVENTION: DISORDERS AND LEUKEMIA, AND USES THEREOF
; FILE REFERENCE: 2320-1-001PCT
; CURRENT APPLICATION NUMBER: US/09/720,934
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/082,007
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-720-934-101

Query Match 36.4%; Score 4; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 4
PCT-US01-27692A-138
; Sequence 138, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 138
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(3)
; OTHER INFORMATION: synthetic construct
PCT-US01-27692A-138

Query Match 36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 3 L 3

RESULT 5
PCT-US01-27692A-142
; Sequence 142, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(3)
; OTHER INFORMATION: synthetic construct
PCT-US01-27692A-142

Query Match 36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 1 L 1

RESULT 6
PCT-US01-27692A-161
; Sequence 161, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(3)
; OTHER INFORMATION: synthetic construct
PCT-US01-27692A-161

Query Match 36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 3 L 3

RESULT 7
PCT-US01-27692A-179
; Sequence 179, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251

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;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 179
;   LENGTH: 3
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(3)
;   OTHER INFORMATION: synthetic construct
PCT-US01-27692A-179


  Query Match             36.4%;  Score 4;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 L 2


RESULT   8
PCT-US01-27692A-181
; Sequence 181, Application PC/TUS0127692A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
;  FILE REFERENCE: 005774.P003PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/27692A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 251
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 181
;   LENGTH: 3
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(3)
;   OTHER INFORMATION: synthetic construct
PCT-US01-27692A-181


  Query Match             36.4%;  Score 4;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 L 2


RESULT   9
PCT-US01-28044A-8
; Sequence 8, Application PC/TUS0128044A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Compositions and Methods for Targeting Peptide in Human In Vivo
;  FILE REFERENCE: 005774.P002PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28044A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 423
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 3
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(3)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28044A-8


  Query Match             36.4%;  Score 4;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT  10
PCT-US01-28044A-9
; Sequence 9, Application PC/TUS0128044A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Compositions and Methods for Targeting Peptide in Human In Viv
;  FILE REFERENCE: 005774.P002PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28044A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 423
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 3
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(3)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28044A-9


  Query Match             36.4%;  Score 4;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT  11
PCT-US01-28044A-10
; Sequence 10, Application PC/TUS0128044A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Compositions and Methods for Targeting Peptide in Human In Viv
;  FILE REFERENCE: 005774.P002PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28044A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 423
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 3
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(3)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28044A-10


  Query Match             36.4%;  Score 4;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT  12
```

```
PCT-US01-28044A-15
; Sequence 15, Application PC/TUS0128044A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Compositions and Methods for Targeting Peptide in Human In Vivo
;  FILE REFERENCE: 005774.P002PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28044A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 423
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 3
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(3)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28044A-15


  Query Match             36.4%;  Score 4;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       3 L 3


RESULT  13
PCT-US01-28044A-21
; Sequence 21, Application PC/TUS0128044A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Compositions and Methods for Targeting Peptide in Human In Vivo
;  FILE REFERENCE: 005774.P002PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28044A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 423
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
;   LENGTH: 3
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(3)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28044A-21


  Query Match             36.4%;  Score 4;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       3 L 3


RESULT  14
PCT-US01-28044A-130
; Sequence 130, Application PC/TUS0128044A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Compositions and Methods for Targeting Peptide in Human In Vivo
;  FILE REFERENCE: 005774.P002PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28044A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 423
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
;   LENGTH: 3
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(3)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28044A-130


  Query Match             36.4%;  Score 4;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       1 L 1


RESULT  15
PCT-US01-28044A-306
; Sequence 306, Application PC/TUS0128044A
; GENERAL INFORMATION:
;  APPLICANT: Board of Regents, The University of Texas System
;  TITLE OF INVENTION: Compositions and Methods for Targeting Peptide in Human In Viv
;  FILE REFERENCE: 005774.P002PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/28044A
;  CURRENT FILING DATE:  2001-09-07
;  NUMBER OF SEQ ID NOS: 423
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 306
;   LENGTH: 3
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: (1)..(3)
;   OTHER INFORMATION: synthetic construct
PCT-US01-28044A-306


  Query Match             36.4%;  Score 4;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       1 L 1


Search completed: December 13, 2001, 10:49:47
Job time: 307 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 11:55:36 ; Search time 20.43 Seconds
(without alignments)
8.812 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 8027

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	8	2	US-08-669-284B-30	Sequence 30, Appl
2	21	50.0	8	4	US-08-444-818-659	Sequence 659, App
3	20	47.6	8	1	US-08-178-570-47	Sequence 47, Appl
4	20	47.6	8	3	US-08-369-643-47	Sequence 47, Appl
5	20	47.6	8	5	PCT-US95-00147-47	Sequence 47, Appl
6	19	45.2	8	1	US-08-178-570-48	Sequence 48, Appl
7	19	45.2	8	3	US-08-369-643-48	Sequence 48, Appl
8	19	45.2	8	5	PCT-US95-00147-48	Sequence 48, Appl
9	19	45.2	8	6	5258287-44	Patent No. 5258287
10	18	42.9	8	1	US-08-082-847-7	Sequence 7, Appli
11	18	42.9	8	1	US-08-082-847-9	Sequence 9, Appli
12	18	42.9	8	1	US-08-082-847-29	Sequence 29, Appl
13	18	42.9	8	1	US-08-375-962B-2	Sequence 2, Appli
14	18	42.9	8	1	US-08-615-181-67	Sequence 67, Appl
15	18	42.9	8	2	US-08-978-404B-62	Sequence 62, Appl
16	18	42.9	8	2	US-08-562-114B-2	Sequence 2, Appli
17	18	42.9	8	3	US-08-478-208-18	Sequence 18, Appl
18	18	42.9	8	4	US-08-444-818-734	Sequence 734, App
19	18	42.9	8	4	US-08-444-818-735	Sequence 735, App
20	18	42.9	8	4	US-08-444-818-736	Sequence 736, App
21	18	42.9	8	4	US-08-444-818-737	Sequence 737, App
22	18	42.9	8	4	US-08-861-423A-9	Sequence 9, Appli
23	18	42.9	8	4	US-07-861-458C-121	Sequence 121, App
24	18	42.9	8	4	US-08-729-594A-2	Sequence 2, Appli
25	18	42.9	8	5	PCT-US95-02140-1	Sequence 1, Appli
26	17	40.5	8	1	US-08-236-240-3	Sequence 3, Appli
27	17	40.5	8	1	US-08-266-514-12	Sequence 12, Appl
28	17	40.5	8	2	US-08-654-604-12	Sequence 12, Appl
29	17	40.5	8	2	US-08-934-222-140	Sequence 140, App
30	17	40.5	8	2	US-08-669-284B-13	Sequence 13, Appl
31	17	40.5	8	2	US-08-669-284B-14	Sequence 14, Appl
32	17	40.5	8	2	US-08-669-284B-15	Sequence 15, Appl
33	17	40.5	8	2	US-08-933-402-140	Sequence 140, App
34	17	40.5	8	2	US-09-207-621-140	Sequence 140, App
35	17	40.5	8	2	US-08-350-260A-466	Sequence 466, App
36	17	40.5	8	2	US-08-532-818-140	Sequence 140, App
37	17	40.5	8	3	US-09-231-797-140	Sequence 140, App
38	17	40.5	8	3	US-08-934-224-140	Sequence 140, App
39	17	40.5	8	3	US-08-933-843-140	Sequence 140, App
40	17	40.5	8	4	US-08-934-223-140	Sequence 140, App
41	17	40.5	8	4	US-08-444-818-660	Sequence 660, App
42	17	40.5	8	4	US-09-171-654-23	Sequence 23, Appl
43	17	40.5	8	4	US-09-413-492-140	Sequence 140, App
44	16	38.1	8	1	US-08-178-570-50	Sequence 50, Appl
45	16	38.1	8	1	US-08-259-550A-30	Sequence 30, Appl

ALIGNMENTS

```
RESULT 1
US-08-669-284B-30
; Sequence 30, Application US/08669284B
; Patent No. 5939534
;  GENERAL INFORMATION:
;    APPLICANT:  Inoue, Makoto
;    APPLICANT:  Kikuchi, Kaoru
;    APPLICANT:  Ishige, Yoko
;    APPLICANT:  Ito, Akira
;    APPLICANT:  Kimura, Toru
;    APPLICANT:  Nakayama, Chikao
;    APPLICANT:  No. 5939534uchi, Hiroshi
;    TITLE OF INVENTION:  NOVEL HUMAN CILIARY NEUROTROPHIC FACTORS
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/669,284B
;      FILING DATE:  28-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP94/02269
;      FILING DATE:  27-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 06-268281
;      FILING DATE:  05-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 06-201504
;      FILING DATE:  02-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 05-350934
;      FILING DATE:  29-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nakamura, Dean H.
;      REGISTRATION NUMBER:  33,981
;      REFERENCE/DOCKET NUMBER:  Q-42041
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)293-7060
;      TELEFAX:  (202)293-7860
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
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SEQ ID NO:30

; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-669-284B-30

Query Match 100.0%; Score 42; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 1 LTEKKYSP 8

RESULT 2
US-08-444-818-659
; Sequence 659, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 659:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-444-818-659

Query Match 50.0%; Score 21; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LTEKKY 6
|||: |
Db 1 LTERLY 6

RESULT 3
US-08-178-570-47

; Sequence 47, Application US/08178570
; Patent No. 5532167
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-178-570-47

Query Match 47.6%; Score 20; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EKKYSP 8
|::| |
Db 1 EEEYMP 6

RESULT 4
US-08-369-643-47
; Sequence 47, Application US/08369643A
; Patent No. 6004757
; GENERAL INFORMATION:
; APPLICANT: Cantley, Lewis C.
; APPLICANT: Songyang, Zhou
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; FILE REFERENCE: CNS-001CP
; CURRENT APPLICATION NUMBER: US/08/369,643A
; CURRENT FILING DATE: 1995-01-06
; EARLIER APPLICATION NUMBER: US 08/178,570
; EARLIER FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Mouse polyoma
; OTHER INFORMATION: middle T (Y315)
US-08-369-643-47

```
 Query Match             47.6%;  Score 20;  DB 3;  Length 8;
 Best Local Similarity   50.0%;  Pred. No. 1.6e+05;
 Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 EKKYSP 8
           |::| |
Db       1 EEEYMP 6


RESULT   5
PCT-US95-00147-47
; Sequence 47, Application PC/TUS9500147
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Substrate Specificity of Protein Kinases
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, suite 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/00147
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/178,570
;      FILING DATE:  JANUARY 7, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A., Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  BBI-004CPPC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  47:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
PCT-US95-00147-47


  Query Match             47.6%;  Score 20;  DB 5;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.6e+05;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 EKKYSP 8
           |::| |
Db       1 EEEYMP 6


RESULT   6
US-08-178-570-48
; Sequence 48, Application US/08178570
; Patent No. 5532167
;  GENERAL INFORMATION:
;    APPLICANT:  Lewis C. Cantley
;    APPLICANT:  Zhou Song yang
;    TITLE OF INVENTION:  Substrate Specificity of Protein Kinases
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, suite 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/178,570
;      FILING DATE:  JANUARY 7, 1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A., Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  BBI-004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-08-178-570-48


  Query Match             45.2%;  Score 19;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.6e+05;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 EKKYSP 8
           | :| |
Db       1 ENEYMP 6


RESULT   7
US-08-369-643-48
; Sequence 48, Application US/08369643A
; Patent No. 6004757
; GENERAL INFORMATION:
;  APPLICANT: Cantley, Lewis C.
;  APPLICANT: Songyang, Zhou
;  TITLE OF INVENTION: Substrate Specificity of Protein Kinases
;  FILE REFERENCE: CNS-001CP
;  CURRENT APPLICATION NUMBER: US/08/369,643A
;  CURRENT FILING DATE: 1995-01-06
;  EARLIER APPLICATION NUMBER: US 08/178,570
;  EARLIER FILING DATE: 1994-01-07
;  NUMBER OF SEQ ID NOS: 92
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hamster
;   OTHER INFORMATION: polyoma middle T (Y295)
US-08-369-643-48


  Query Match             45.2%;  Score 19;  DB 3;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.6e+05;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 EKKYSP 8
           | :| |
Db       1 ENEYMP 6
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RESULT   8
PCT-US95-00147-48
; Sequence 48, Application PC/TUS9500147
;  GENERAL INFORMATION:
;     APPLICANT:
;     TITLE OF INVENTION:  Substrate Specificity of Protein Kinases
;     NUMBER OF SEQUENCES:  88
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  LAHIVE & COCKFIELD
;       STREET:  60 STATE STREET, suite 510
;       CITY:  BOSTON
;       STATE:  MASSACHUSETTS
;       COUNTRY:  USA
;       ZIP:  02109-1875
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  ASCII text
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/00147
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/178,570
;       FILING DATE:  JANUARY 7, 1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DeConti, Giulio A., Jr.
;       REGISTRATION NUMBER:  31,503
;       REFERENCE/DOCKET NUMBER:  BBI-004CPPC
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 227-7400
;       TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  48:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FRAGMENT TYPE:  internal
PCT-US95-00147-48


  Query Match             45.2%;  Score 19;  DB 5;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.6e+05;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 EKKYSP 8
           | :| |
Db       1 ENEYMP 6


RESULT   9
5258287-44
;Patent No. 5258287
;     APPLICANT: BAXTER, ROBERT C.;WOOD, WILLIAM I.
;     TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION
;OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53
;     NUMBER OF SEQUENCES: 58
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/171,623
;       FILING DATE: 22-MAR-1988
;SEQ ID NO:44:
;       LENGTH: 8
5258287-44


  Query Match             45.2%;  Score 19;  DB 6;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.6e+05;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 EKKYSP 8
           | :| |
Db       1 ETEYGP 6


RESULT  10
US-08-082-847-7
; Sequence 7, Application US/08082847
; Patent No. 5492894
;  GENERAL INFORMATION:
;     APPLICANT:  FULMER, ANDREW W.
;     APPLICANT:  BASCOM, CHARLES C.
;     TITLE OF INVENTION:  COMPOSITIONS FOR REGULATING WRINKLES
;     TITLE OF INVENTION:  COMPRISING A PEPTIDE
;     NUMBER OF SEQUENCES:  38
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  THE PROCTER & GAMBLE COMPANY
;       STREET:  P. O. BOX 398707
;       CITY:  CINCINNATI
;       STATE:  OHIO
;       COUNTRY:  USA
;       ZIP:  45239-8707
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/082,847
;       FILING DATE:  19930625
;       CLASSIFICATION:  530
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  CORSTANJE, BRAHM J.
;       REGISTRATION NUMBER:  34,804
;       REFERENCE/DOCKET NUMBER:  4346CR
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  513-627-2858
;       TELEFAX:  513-627-0260
;  INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-082-847-7


  Query Match             42.9%;  Score 18;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 1.6e+05;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KKYS 7
           :|||
Db       5 RKYS 8


RESULT  11
US-08-082-847-9
; Sequence 9, Application US/08082847
; Patent No. 5492894
;  GENERAL INFORMATION:
;     APPLICANT:  FULMER, ANDREW W.
;     APPLICANT:  BASCOM, CHARLES C.
;     TITLE OF INVENTION:  COMPOSITIONS FOR REGULATING WRINKLES
;     TITLE OF INVENTION:  COMPRISING A PEPTIDE
;     NUMBER OF SEQUENCES:  38
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  THE PROCTER & GAMBLE COMPANY
;       STREET:  P. O. BOX 398707
;       CITY:  CINCINNATI
;       STATE:  OHIO
;       COUNTRY:  USA
;       ZIP:  45239-8707
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,847
; FILING DATE: 19930625
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 4346CR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-627-2858
; TELEFAX: 513-627-0260
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-082-847-9

Query Match 42.9%; Score 18; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKYS 7
:|||
Db 5 RKYS 8

RESULT 12
US-08-082-847-29
; Sequence 29, Application US/08082847
; Patent No. 5492894
; GENERAL INFORMATION:
; APPLICANT: FULMER, ANDREW W.
; APPLICANT: BASCOM, CHARLES C.
; TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES
; TITLE OF INVENTION: COMPRISING A PEPTIDE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER & GAMBLE COMPANY
; STREET: P. O. BOX 398707
; CITY: CINCINNATI
; STATE: OHIO
; COUNTRY: USA
; ZIP: 45239-8707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,847
; FILING DATE: 19930625
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 4346CR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-627-2858
; TELEFAX: 513-627-0260
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-082-847-29

Query Match 42.9%; Score 18; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKYS 7
:|||
Db 4 RKYS 7

RESULT 13
US-08-375-962B-2
; Sequence 2, Application US/08375962B
; Patent No. 5731195
; GENERAL INFORMATION:
; APPLICANT: SIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT,
; APPLICANT: CHRISTER; ERIKSSON, ULF.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecule
; TITLE OF INVENTION: Which Codes for A 32 kDa Protein Having 11-CIS Retinol
; TITLE OF INVENTION: Dehydrogenase Activity, and Which Associates With P63,
; TITLE OF INVENTION: a Portion of a Retinol Binding Protein Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pelfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect (ASCII standard)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/375,962B
; FILING DATE: 20-January-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/258,418
; FILING DATE: 6-October-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-375-962B-2

Query Match 42.9%; Score 18; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YSP 8
|||
Db 1 YSP 3

RESULT 14
US-08-615-181-67
; Sequence 67, Application US/08615181
; Patent No. 5756666
; GENERAL INFORMATION:
; APPLICANT: MASAFUMI, TAKIGUCHI
; APPLICANT: MIWA, KIYOSHI
; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE

```
;    TITLE OF INVENTION:  RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND
;    TITLE OF INVENTION:  CURING AIDS
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/615,181
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP94/01756
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 261302/1993
;      FILING DATE:  19-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  10-796-0 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  67:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  HUMAN IMMUNODEFICIENCY VIRUS
US-08-615-181-67


  Query Match             42.9%;  Score 18;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 1.6e+05;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 EKKY 6
           :|||
Db       5 KKKY 8


RESULT  15
US-08-978-404B-62
; Sequence 62, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  62:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 5968782e
US-08-978-404B-62


  Query Match             42.9%;  Score 18;  DB 2;  Length 8;
  Best Local Similarity   57.1%;  Pred. No. 1.6e+05;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 TEKKYSP 8
             |  | ||
Db       2 TPTKLSP 8


Search completed: December 13, 2001, 11:56:05
Job time: 29 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:44:40 ; Search time 22.81 Seconds
(without alignments)
26.716 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	72	2	I79343	interferon alpha T
2	42	100.0	167	2	E25843	interferon alpha-F
3	42	100.0	167	2	D25843	interferon alpha-G
4	42	100.0	176	2	I56314	interferon-alpha -
5	42	100.0	181	2	I56313	interferon alpha 2
6	42	100.0	189	1	IVHUI6	interferon alpha-I
7	42	100.0	189	1	IVHUA7	interferon alpha-5
8	42	100.0	189	1	IVHUA1	interferon alpha-1
9	42	100.0	189	1	IVHUF	interferon alpha-I
10	42	100.0	189	1	IVHU4B	interferon alpha-I
11	42	100.0	189	1	IVHUA9	interferon alpha-1
12	42	100.0	189	2	I52347	interferon alpha-M
13	42	100.0	189	2	I84464	interferon-alpha-F
14	42	100.0	189	2	I53102	interferon-alpha-J
15	42	100.0	189	2	I51970	interferon precurs
16	36	85.7	165	2	I78570	alpha 2 interferon
17	36	85.7	167	2	F25843	interferon alpha-J
18	36	85.7	170	2	A48772	interferon, atypic
19	36	85.7	184	1	IVHOA4	interferon alpha-I
20	36	85.7	184	1	IVHOA2	interferon alpha-I
21	36	85.7	184	1	IVHOA3	interferon alpha-I
22	36	85.7	184	1	IVHOA1	interferon alpha-I
23	36	85.7	188	1	IVHUA2	interferon alpha-2
24	36	85.7	189	1	IVHU14	interferon alpha-I
25	36	85.7	189	1	IVHUA0	interferon alpha-7
26	36	85.7	194	2	JS0664	interferon precurs
27	36	85.7	730	2	H86295	hypothetical prote
28	35	83.3	162	2	C25843	interferon alpha-B
29	35	83.3	189	1	IVHUA4	interferon alpha-4
30	35	83.3	189	1	IVHUI8	interferon alpha-I
31	35	83.3	195	1	IVHO21	interferon alpha-I
32	33	78.6	110	2	F85431	hypothetical prote
33	33	78.6	189	1	IVHUA5	interferon alpha-5
34	33	78.6	221	2	D86051	hypothetical prote
35	32	76.2	114	2	S69147	immunomodulatory p
36	32	76.2	414	2	D96524	protein T1N15.3 [i
37	32	76.2	573	2	T27578	hypothetical prote
38	32	76.2	1528	2	T37308	ATPase homolog - C
39	31	73.8	189	1	IVMSA5	interferon alpha-I
40	31	73.8	189	1	IVMSA1	interferon alpha-I
41	31	73.8	189	1	IVMSA6	interferon alpha-I
42	31	73.8	189	2	S23709	interferon alpha-1
43	31	73.8	189	2	I49773	murine interferon
44	31	73.8	190	1	IVMSA2	interferon alpha-2
45	31	73.8	190	2	JH0468	interferon alpha-1

ALIGNMENTS

RESULT 1
I79343
interferon alpha T - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 16-Jul-1999
C;Accession: I79343
R;Lund, B.; Edlund, T.; Lindenmaier, W.; Ny, T.; Collins, J.; Lundgren, E.; von Gabai
Proc. Natl. Acad. Sci. U.S.A. 81, 2435-2439, 1984
A;Title: Novel cluster of alpha-interferon gene sequences in a placental cosmid DNA l
A;Reference number: I58999; MUID:84194022
A;Accession: I79343
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-72 <RES>
A;Cross-references: GB:K01461; NID:g184575; PIDN:AAA58685.1; PID:g184579
C;Superfamily: interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 65 LTEKKYSP 72

RESULT 2
E25843
interferon alpha-F - human
N;Alternate names: human leukocyte interferon (IFN)
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 15-Jun-1996
C;Accession: E25843
R;Ohara, O.; Teraoka, H.
FEBS Lett. 211, 78-82, 1987
A;Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide
A;Reference number: A91374; MUID:87105954
A;Accession: E25843
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-167 <OHA>
C;Superfamily: interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 132 LTEKKYSP 139

RESULT 3
D25843
interferon alpha-G - human
N;Alternate names: human leukocyte interferon (IFN)
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 15-Jun-1996
C;Accession: D25843
R;Ohara, O.; Teraoka, H.
FEBS Lett. 211, 78-82, 1987
A;Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide gel
A;Reference number: A91374; MUID:87105954
A;Accession: D25843
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-167 <OHA>
C;Superfamily: interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 132 LTEKKYSP 139

RESULT 4
I56314
interferon-alpha - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I56314
R;Lund, B.; von Gabain, A.; Edlund, T.; Ny, T.; Lundgren, E.
J. Interferon Res. 5, 229-238, 1985
A;Title: Differential expression of interferon genes in a substrain of Namalwa cells.
A;Reference number: I56314; MUID:85235859
A;Accession: I56314
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-176 <RES>
A;Cross-references: GB:M71246; NID:g184572; PIDN:AAA52713.1; PID:g184573
C;Genetics:
A;Gene: IFNA
C;Superfamily: interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 141 LTEKKYSP 148

RESULT 5
I56313
interferon alpha 21 - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I56313
R;Gren, E.; Berzin, V.M.; Jansone, I.; Tsimanis, A.; Vishnevsky, Y.; Apsalons, U.
J. Interferon Res. 4, 609-617, 1984
A;Title: Novel human leukocyte interferon subtype and structural comparison of alpha int
A;Reference number: I56313; MUID:85056523
A;Accession: I56313
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-181 <RES>
A;Cross-references: GB:M28586; NID:g184636; PIDN:AAA36041.1; PID:g306912
C;Genetics:
A;Gene: GDB:IFNA21
A;Cross-references: GDB:136360; OMIM:147584
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 146 LTEKKYSP 153

RESULT 6
IVHUI6
interferon alpha-I-6 precursor - human
N;Alternate names: HuIFN-alpha-I-6; LeIF K; type I interferon
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999
C;Accession: A23753
R;Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.;
J. Mol. Biol. 185, 227-260, 1985
A;Title: Structural relationship of human interferon alpha genes and pseudogenes.
A;Reference number: A92916; MUID:86037205
A;Accession: A23753
A;Molecule type: DNA
A;Residues: 1-189 <HEN>
A;Cross-references: GB:X02958; NID:g32662; PIDN:CAA26704.1; PID:g758080
C;Genetics:
A;Gene: GDB:IFNA6
A;Cross-references: GDB:136363; OMIM:147566
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: antiviral
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-I-6 #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted

Query Match 100.0%; Score 42; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 154 LTEKKYSP 161

RESULT 7
IVHUA7
interferon alpha-5 precursor - human
N;Alternate names: interferon alpha-G
C;Species: Homo sapiens (man)
C;Date: 01-Sep-1981 #sequence_revision 29-Jan-1999 #text_change 21-Jul-2000
C;Accession: S43716; A01833
R;Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.;
J. Mol. Biol. 185, 227-260, 1985
A;Title: Structural relationship of human interferon alpha genes and pseudogenes.
A;Reference number: A92916; MUID:86037205
A;Accession: S43716
A;Molecule type: DNA
A;Residues: 1-189 <HEN>
A;Cross-references: EMBL:X02956; NID:g32659; PIDN:CAA26702.1; PID:g758079
R;Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeb
Nature 290, 20-26, 1981
A;Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.
A;Reference number: A93249; MUID:81148795
A;Accession: A01833
A;Molecule type: mRNA
A;Residues: 57-189 <GOE>

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A;Cross-references: GB:V00541; GB:J00213; NID:g32718; PIDN:CAA23802.1; PID:g32719
A;Note: eight classes of interferon alpha clones were identified; this sequence is deriv
C;Genetics:
A;Gene: GDB:IFNA5
A;Cross-references: GDB:136362; OMIM:147565
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: antiviral; cytokine; leukocyte
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-5 #status predicted <MAT>


  Query Match             100.0%;  Score 42;  DB 1;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    154 LTEKKYSP 161


RESULT   8
IVHUA1
interferon alpha-1 precursor - human
N;Alternate names: interferon alpha-13; interferon alpha-D; interferon alpha-I-1
C;Species: Homo sapiens (man)
C;Date: 22-May-1981 #sequence_revision 01-Sep-1981 #text_change 24-Sep-1999
C;Accession: C23285; A91467; A93226; A93249; I58213; S43715; S41196; A01826
R;Capon, D.J.; Shepard, H.M.; Goeddel, D.V.
Mol. Cell. Biol. 5, 768-779, 1985
A;Title: Two distinct families of human and bovine interferon-alpha genes are coordinate
A;Reference number: A93070; MUID:85187974
A;Accession: C23285
A;Molecule type: DNA
A;Residues: 1-189 <CAP>
R;Mantei, N.; Schwarzstein, M.; Streuli, M.; Panem, S.; Nagata, S.; Weissmann, C.
Gene 10, 1-10, 1980
A;Title: The nucleotide sequence of a cloned human leukocyte inteferon cDNA.
A;Reference number: A91467; MUID:81005094
A;Accession: A91467
A;Molecule type: mRNA
A;Residues: 1-189 <MAN>
A;Cross-references: GB:V00537; NID:g32711; PIDN:CAA23798.1; PID:g32712
R;Taniguchi, T.; Mantei, N.; Schwarzstein, M.; Nagata, S.; Muramatsu, M.; Weissmann, C.
Nature 285, 547-549, 1980
A;Title: Human leukocyte and fibroblast interferons are structurally related.
A;Reference number: A93226; MUID:80254543
A;Accession: A93226
A;Molecule type: mRNA
A;Residues: 1-189 <TAN>
R;Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeburg
Nature 290, 20-26, 1981
A;Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.
A;Reference number: A93249; MUID:81148795
A;Accession: A93249
A;Molecule type: mRNA
A;Residues: 1-136,'V',138-189 <GOE>
A;Cross-references: GB:V00538; NID:g32713; PIDN:CAA23799.1; PID:g32714
A;Note: eight classes of interferon alpha clones were identified; this sequence is deriv
R;Weber, H.; Weissmann, C.
Nucleic Acids Res. 11, 5661-5669, 1983
A;Title: Formation of genes coding for hybrid proteins by recombination between related,
A;Reference number: I58213; MUID:83299241
A;Accession: I58213
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 24-189 <RES>
A;Cross-references: GB:M29884; NID:g184583; PIDN:AAA52714.1; PID:g386794
R;Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov
J. Mol. Biol. 185, 227-260, 1985
A;Title: Structural relationship of human interferon alpha genes and pseudogenes.
A;Reference number: A92916; MUID:86037205
A;Accession: S43715
A;Molecule type: DNA
A;Residues: 1-189 <HEN>
A;Cross-references: EMBL:X75934
R;Rostoks, N.
submitted to the EMBL Data Library, December 1993
A;Reference number: S41196
A;Accession: S41196
A;Molecule type: DNA
A;Residues: 1-9,'A',11-189 <ROS>
A;Cross-references: EMBL:X75934; NID:g439666; PIDN:CAA53538.1; PID:g439667
C;Genetics:
A;Gene: GDB:IFNA1
A;Cross-references: GDB:136353; OMIM:147660
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: antiviral; cytokine; leukocyte
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-1 #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted


  Query Match             100.0%;  Score 42;  DB 1;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    154 LTEKKYSP 161


RESULT   9
IVHUF
interferon alpha-I-F precursor - human
N;Alternate names: HuIFN-alpha-I-F; LeIF F; type I interferon
C;Species: Homo sapiens (man)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 28-May-1999
C;Accession: A01832
R;Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeb
Nature 290, 20-26, 1981
A;Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.
A;Reference number: A93249; MUID:81148795
A;Accession: A01832
A;Molecule type: mRNA
A;Residues: 1-189 <GOE>
A;Cross-references: GB:V00540; GB:J00212; NID:g32716; PIDN:CAA23801.1; PID:g32717
A;Note: eight classes of interferon alpha clones were identified; this sequence is de
C;Genetics:
A;Gene: GDB:IFN1@
A;Cross-references: GDB:119328; OMIM:147660
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: antiviral
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-I-F #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted


  Query Match             100.0%;  Score 42;  DB 1;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    154 LTEKKYSP 161


RESULT  10
IVHU4B
interferon alpha-I-4b precursor - human
N;Alternate names: HuIFN-alpha-I-4b; type I interferon
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999
C;Accession: E23753
```

R;Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov
J. Mol. Biol. 185, 227-260, 1985
A;Title: Structural relationship of human interferon alpha genes and pseudogenes.
A;Reference number: A92916; MUID:86037205
A;Accession: E23753
A;Molecule type: DNA
A;Residues: 1-189 <HEN>
A;Cross-references: GB:X02955; NID:g32656; PIDN:CAA26701.1; PID:g758078
C;Genetics:
A;Gene: GDB:IFN1@
A;Cross-references: GDB:119328; OMIM:147660
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: antiviral
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-I-4b #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted

Query Match 100.0%; Score 42; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 154 LTEKKYSP 161

RESULT 11
IVHUA9
interferon alpha-17 precursor - human
N;Alternate names: interferon alpha-9; interferon alpha-I'
C;Species: Homo sapiens (man)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jul-2000
C;Accession: A01835; A22255; C42753
R;Lawn, R.M.; Adelman, J.; Dull, T.J.; Gross, M.; Goeddel, D.; Ullrich, A.
Science 212, 1159-1162, 1981
A;Title: DNA sequence of two closely linked human leukocyte interferon genes.
A;Reference number: A94255; MUID:81201124
A;Accession: A01835
A;Molecule type: DNA
A;Residues: 1-189 <LAW>
A;Cross-references: GB:J00216; GB:V00532; NID:g32633; PIDN:CAA23793.1; PID:g32634
R;Mizoguchi, J.; Pitha, P.M.; Raj, N.B.K.
DNA 4, 221-232, 1985
A;Title: Efficient expression in Escherichia coli of two species of human interferon-alp
A;Reference number: A22255; MUID:85229953
A;Accession: A22255
A;Molecule type: mRNA
A;Residues: 1-56,'H',58-189 <MIZ>
A;Cross-references: GB:M11026; NID:g184612; PIDN:AAA52725.1; PID:g306908
R;Zoon, K.C.; Miller, D.; Bekisz, J.; zur Nedden, D.; Enterline, J.C.; Nguyen, N.Y.; Hu,
J. Biol. Chem. 267, 15210-15216, 1992
A;Title: Purification and characterization of multiple components of human lymphoblastoi
A;Reference number: A42753; MUID:92340576
A;Accession: C42753
A;Molecule type: protein
A;Residues: 'X',25-50,'XX',53-56 <ZOO>
C;Genetics:
A;Gene: GDB:IFNA17
A;Cross-references: GDB:136358; OMIM:147583
A;Map position: 9p22-9p22
C;Superfamily: interferon alpha
C;Keywords: leukocyte
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-189/Product: interferon alpha-17 #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted

Query Match 100.0%; Score 42; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 154 LTEKKYSP 161

RESULT 12
I52347
interferon alpha-M1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I52347
R;Linnane, A.W.; Beilharz, M.W.; McMullen, G.L.; Macreadie, I.G.; Murphy, M.; Nisbet,
Biochem. Int. 8, 725-732, 1984
A;Title: Nucleotide sequence and expression in E. coli of a human interferon-alpha ge
A;Reference number: I52347; MUID:84307815
A;Accession: I52347
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-189 <RES>
A;Cross-references: GB:M27318; NID:g184617; PIDN:AAA52726.1; PID:g306909
C;Genetics:
A;Gene: IFNA
C;Superfamily: interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 154 LTEKKYSP 161

RESULT 13
I84464
interferon-alpha-F - human
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C;Accession: I84464; I37583
R;Gren, E.Y.; Berzin, V.M.; Tsimanis, A.Y.; Apsalon, U.R.; Vishnevskii, Y.I.; Yansone
.A.; Lozha, V.P.; Kavsan, V.M.; Efimov, V.A.; Sverdlov, E.D.
Dokl. Biochem. 269, 91-95, 1983
A;Title: A new type of leukocytic interferon.
A;Reference number: I37583
A;Accession: I84464
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-189 <RES>
A;Cross-references: GB:M12350; NID:g184598; PIDN:AAA52718.1; PID:g306906
A;Accession: I37583
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-189 <RE2>
A;Cross-references: EMBL:X00145; NID:g32724; PIDN:CAA24980.1; PID:g32725
C;Genetics:
A;Gene: IFNA
C;Superfamily: interferon alpha

Query Match 100.0%; Score 42; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 154 LTEKKYSP 161

RESULT 14
I53102
interferon-alpha-J1 - human
C;Species: Homo sapiens (man)

```
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I53102
R;Cohen, S.; Velan, B.; Grosfeld, H.; Shalita, Z.; Leitner, M.; Shafferman, A.
Dev. Biol. Stand. 60, 111-122, 1985
A;Title: Cloning, expression and biological activity of a new variant of human interferc
A;Reference number: I53102; MUID:86005847
A;Accession: I53102
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-189 <RES>
A;Cross-references: GB:M34913; NID:g184614; PIDN:AAA36039.1; PID:g184615
C;Superfamily: interferon alpha


  Query Match             100.0%;  Score 42;  DB 2;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db     154 LTEKKYSP 161


RESULT  15
I51970
interferon precursor - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I51970
R;Saveliev, V.I.; Zlochevsky, M.L.; Sorokin, A.V.; Naroditskaya, V.A.; Bolotin, A.P.; De
Antibiot. Med. Biotekhnol. 31, 592-596, 1986
A;Title: [Cloning and the determination of the nucleotide sequences in 2 genes of human
A;Reference number: I51970; MUID:87024453
A;Accession: I51970
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-189 <RES>
A;Cross-references: GB:M38289; NID:g186407; PIDN:AAA59165.1; PID:g186408
C;Genetics:
A;Gene: IFNA
C;Superfamily: interferon alpha


  Query Match             100.0%;  Score 42;  DB 2;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db     154 LTEKKYSP 161



Search completed: December 13, 2001, 10:45:38
Job time: 58 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 11:56:12 ; Search time 34.38 Seconds
(without alignments)
34.037 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 287

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	25	59.5	8	2	Q9R9E0	Q9r9e0 bacillus su
2	14	33.3	8	8	Q9TMN4	Q9tmn4 begonia for
3	14	33.3	8	8	Q9T2Y2	Q9t2y2 begonia tai
4	14	33.3	8	8	Q9T2Y1	Q9t2y1 begonia apt
5	14	33.3	8	10	Q9XGL9	Q9xgl9 begonia nan
6	14	33.3	8	10	Q9XGL8	Q9xgl8 begonia chi
7	14	33.3	8	10	Q9STD5	Q9std5 begonia pal
8	13	31.0	8	2	Q9R7T2	Q9r7t2 escherichia
9	13	31.0	8	12	Q84271	Q84271 human papil
10	12	28.6	8	6	Q9XSY1	Q9xsy1 canis famil
11	12	28.6	8	8	Q35792	Q35792 saccharomyc
12	12	28.6	8	11	Q62933	Q62933 rattus norv
13	11	26.2	8	2	Q56429	Q56429 thermus aqu
14	11	26.2	8	2	Q9R5L7	Q9r517 clostridium
15	11	26.2	8	4	Q15895	Q15895 homo sapien
16	11	26.2	8	5	P82689	P82689 periplaneta
17	11	26.2	8	6	P82929	P82929 bos taurus
18	11	26.2	8	6	Q9BFA7	Q9bfa7 macroscelid
19	11	26.2	8	7	Q95213	Q95213 oryctolagus
20	11	26.2	8	8	Q9T2Y3	Q9t2y3 begonia for
21	10	23.8	8	2	Q44463	Q44463 agrobacteri
22	10	23.8	8	2	Q9ZIE9	Q9zie9 neisseria m
23	10	23.8	8	2	Q9R5R0	Q9r5r0 shigella dy
24	10	23.8	8	2	Q9AGP4	Q9agp4 arthrobacte
25	10	23.8	8	8	Q36898	Q36898 nicotiana p
26	10	23.8	8	10	Q9S8Z4	Q9s8z4 spinacia ol
27	10	23.8	8	11	Q62528	Q62528 mus spretus
28	9	21.4	8	2	Q53790	Q53790 streptococc
29	9	21.4	8	2	Q45889	Q45889 clostridium
30	9	21.4	8	2	O87471	O87471 haemophilus
31	9	21.4	8	2	Q9R9C2	Q9r9c2 borrelia bu
32	9	21.4	8	4	Q15901	Q15901 homo sapien
33	9	21.4	8	4	Q16468	Q16468 homo sapien
34	9	21.4	8	4	Q9Y4J4	Q9y4j4 homo sapien
35	9	21.4	8	4	Q9UHK1	Q9uhk1 homo sapien
36	9	21.4	8	5	P82618	P82618 periplaneta
37	9	21.4	8	8	P92422	P92422 psathyrosta
38	9	21.4	8	8	P92219	P92219 australopyr
39	9	21.4	8	8	P92211	P92211 agropyron c
40	9	21.4	8	8	P92215	P92215 amblyopyrum
41	9	21.4	8	8	P92222	P92222 bromus iner
42	9	21.4	8	8	P92227	P92227 crithopsis
43	9	21.4	8	8	P92373	P92373 haynaldia v
44	9	21.4	8	8	P92382	P92382 hordeum bra
45	9	21.4	8	12	Q98YK9	Q98yk9 human immun

ALIGNMENTS

RESULT 1
Q9R9E0
ID Q9R9E0 PRELIMINARY; PRT; 8 AA.
AC Q9R9E0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE STAGE V SPORULATION PROTEIN E (FRAGMENT).
GN SPOVE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=93003529; PubMed=1391053;
RA Henriques A.O., de Lencastre H., Piggot P.J.;
RT "A Bacillus subtilis morphogene cluster that includes spoVE is
RT homologous to the mra region of Escherichia coli.";
RL Biochimie 74:735-748(1992).
DR EMBL; X64258; CAA45556.1; -.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 893 MW; EE75A1A33321B1A6 CRC64;

Query Match 59.5%; Score 25; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.7e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
:|' ||:||
Db 1 MTTKKTSP 8

RESULT 2
Q9TMN4
ID Q9TMN4 PRELIMINARY; PRT; 8 AA.
AC Q9TMN4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

```
DE   RBCL PROTEIN (FRAGMENT).
GN   RBCL.
OS   Begonia formosana.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Cucurbitales; Begoniaceae; Begonia.
OX   NCBI_TaxID=80370;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chiang T.Y.;
RT   "Sequence announcement: rbcL promotor gene in Begonia formosana.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ009597; CAB52119.1; -.
KW   Chloroplast.
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  921 MW;  FA21AB01B6C775B6 CRC64;

  Query Match             33.3%;  Score 14;  DB 8;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 4.7e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 TEKK 5
           || |
Db       5 TETK 8


RESULT   3
Q9T2Y2
ID   Q9T2Y2      PRELIMINARY;      PRT;     8 AA.
AC   Q9T2Y2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RBCL PROTEIN (FRAGMENT).
GN   RBCL.
OS   Begonia taipeiensis.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Cucurbitales; Begoniaceae; Begonia.
OX   NCBI_TaxID=80371;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chiang T.Y.;
RT   "Sequence announcement: rbcL promotor gene in Begonia formosana.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ009602; CAB52129.1; -.
DR   EMBL; AJ009600; CAB52125.1; -.
DR   EMBL; AJ009601; CAB52127.1; -.
KW   Chloroplast.
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  921 MW;  FA21AB01B6C775B6 CRC64;

  Query Match             33.3%;  Score 14;  DB 8;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 4.7e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 TEKK 5
           || |
Db       5 TETK 8


RESULT   4
Q9T2Y1
ID   Q9T2Y1      PRELIMINARY;      PRT;     8 AA.
AC   Q9T2Y1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RBCL PROTEIN (FRAGMENT).
GN   RBCL.
OS   Begonia aptera.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Cucurbitales; Begoniaceae; Begonia.
OX   NCBI_TaxID=71278;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chiang T.Y.;
RT   "Sequence announcement: rbcL promotor gene in Begonia formosana.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ009606; CAB52086.1; -.
DR   EMBL; AJ009603; CAB52080.1; -.
DR   EMBL; AJ009604; CAB52082.1; -.
DR   EMBL; AJ009605; CAB52084.1; -.
KW   Chloroplast.
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  921 MW;  FA21AB01B6C775B6 CRC64;

  Query Match             33.3%;  Score 14;  DB 8;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 4.7e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 TEKK 5
           || |
Db       5 TETK 8


RESULT   5
Q9XGL9
ID   Q9XGL9      PRELIMINARY;      PRT;     8 AA.
AC   Q9XGL9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   ATPB PROTEIN (FRAGMENT).
GN   ATPB.
OS   Begonia nantoensis.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Cucurbitales; Begoniaceae; Begonia.
OX   NCBI_TaxID=78253;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=16296;
RA   Chiang T.Y.;
RT   "Sequence announcement: promotor for cpDNA atpB gene in Begonia
RT   nantoensis.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ007419; CAB45928.1; -.
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  921 MW;  FA21AB01B6C775B6 CRC64;

  Query Match             33.3%;  Score 14;  DB 10;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 4.7e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 TEKK 5
           || |
Db       5 TETK 8


RESULT   6
Q9XGL8
ID   Q9XGL8      PRELIMINARY;      PRT;     8 AA.
AC   Q9XGL8;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   ATPB GENE PROTEIN (FRAGMENT).
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GN   ATPB GENE.
OS   Begonia chitoensis.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Cucurbitales; Begoniaceae; Begonia.
OX   NCBI_TaxID=78254;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=16296;
RA   Chiang T.Y.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ007420; CAB45929.1; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  921 MW;  FA21AB01B6C775B6 CRC64;


  Query Match             33.3%;  Score 14;  DB 10;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 4.7e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 TEKK 5
           || |
Db       5 TETK 8


RESULT   7
Q9STD5
ID   Q9STD5      PRELIMINARY;      PRT;     8 AA.
AC   Q9STD5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RIBULOSE-BISPHOSPHATE CARBOXYLASE LARGE SUBUNIT (FRAGMENT).
GN   RBCL.
OS   Begonia palmata.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Cucurbitales; Begoniaceae; Begonia.
OX   NCBI_TaxID=99386;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=16081;
RA   Chiang T.Y.;
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ007745; CAB53369.1; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  921 MW;  FA21AB01B6C775B6 CRC64;


  Query Match             33.3%;  Score 14;  DB 10;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 4.7e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 TEKK 5
           || |
Db       5 TETK 8


RESULT   8
Q9R7T2
ID   Q9R7T2      PRELIMINARY;      PRT;     8 AA.
AC   Q9R7T2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   HYPOTHETICAL PROTEIN HI0004 (FRAGMENT).
GN   YQFG.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=97061202; PubMed=8905232;
RA   Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA   Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA   Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA   Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA   Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA   Yano M., Horiuchi T.;
RT   "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
RT   to the 12.7-28.0 min Region on the Linkage Map.";
RL   DNA Res. 3:137-155(1996).
DR   EMBL; D90705; BAA35310.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  964 MW;  DF133B1DD04B476A CRC64;


  Query Match             31.0%;  Score 13;  DB 2;  Length 8;
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Qy       1 LTEKK 5
             : ||:
Db       4 IAEKE 8


RESULT   9
Q84271
ID   Q84271      PRELIMINARY;      PRT;     8 AA.
AC   Q84271;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   L1 PROTEIN (FRAGMENT).
OS   Human papillomavirus type 19.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10608;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88089511; PubMed=2826651;
RA   Krubke J., Kraus J., Delius H., Chow L., Broker T.R., Iftner T.,
RA   Pfister H.;
RT   "Genetic relationship among human papillomaviruses associated with
RT   benign and malignant tumours of patients with epidermodysplasia
RT   verruciformis.";
RL   J. Gen. Virol. 68:3091-3103(1987).
DR   EMBL; D00204; BAA00142.1; -.
FT   NON_TER       1 -    1
SQ   SEQUENCE   8 AA;  987 MW;  7F432403240321A8 CRC64;


  Query Match             31.0%;  Score 13;  DB 12;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 4.7e+05;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TEKK 5
             |::|
Db       2 TKRK 5


RESULT  10
Q9XSY1
ID   Q9XSY1      PRELIMINARY;      PRT;     8 AA.
AC   Q9XSY1;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   RETINOBLASTOMA PROTEIN (FRAGMENT).
GN   RB1.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
```

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RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97049323; PubMed=8894053;
RA   Venta P.J., Brouillette J.A., Yuzbasiyan-Gurkan V., Brewer G.J.;
RT   "Gene-specific universal mammalian sequence-tagged sites: application
RT   to the canine genome.";
RL   Biochem. Genet. 34:321-341(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Venta P.J., Cao Y., Alexander L., Yuzbasiyan-Gurkan V.;
RT   "Dinucleotide repeat polymorphism in the canine retinoblastoma (RB1)
RT   gene.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF155737; AAD38807.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  895 MW;  1425BB18676721E3 CRC64;


  Query Match             28.6%;  Score 12;  DB 6;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 4.7e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 KYSP 8
          |: |
Db      1 KHLP 4


RESULT  11
Q35792
ID   Q35792      PRELIMINARY;      PRT;     8 AA.
AC   Q35792;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   OXI3 LOCUS IN YEAST MITOCHONDRION (STRAIN D273-10B) (CODES FOR
DE   CYTOCHROME OXIDASE SUBUNIT 1).
OS   Saccharomyces cerevisiae (Baker's yeast).
OG   Mitochondrion.
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81069885; PubMed=6254986;
RA   Bonitz S.G., Coruzzi G., Thalenfeld B.E., Tzagoloff A., Macino G.;
RT   "Assembly of the mitochondrial membrane system. Structure and
RT   nucleotide sequence of the gene coding for subunit 1 of yeast
RT   cytochrme oxidase.";
RL   J. Biol. Chem. 255:11927-11941(1980).
DR   EMBL; V00694; CAA24063.1; -.
KW   Mitochondrion.
SQ   SEQUENCE   8 AA;  1025 MW;  084693345B5AA337 CRC64;


  Query Match             28.6%;  Score 12;  DB 8;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 4.7e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 KKYS 7
          | |:
Db      2 KDYN 5


RESULT  12
Q62933
ID   Q62933      PRELIMINARY;      PRT;     8 AA.
AC   Q62933;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   HISTONE H10 (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=TESTIS;
RA   Khochbin S., Peretti M.F., Girardot V.;
RL   Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U49737; AAA92724.1; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  850 MW;  F4C771B5B44B01A6 CRC64;


  Query Match             28.6%;  Score 12;  DB 11;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 4.7e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTE 3
          :||
Db      1 MTE 3


RESULT  13
Q56429
ID   Q56429      PRELIMINARY;      PRT;     8 AA.
AC   Q56429;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   GAPDH (FRAGMENT).
OS   Thermus aquaticus (subsp. thermophilus).
OC   Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.
OX   NCBI_TaxID=274;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HB-8;
RX   MEDLINE=89025722; PubMed=3052437;
RA   Bowen D., Littlechild J.A., Fothergill J.E., Watson H.C., Hall L.;
RT   "Nucleotide sequence of the phosphoglycerate kinase gene from the
RT   extreme thermophile Thermus thermophilus. Comparison of the deduced
RT   amino acid sequence with that of the mesophilic yeast phosphoglycerate
RT   kinase.";
RL   Biochem. J. 254:509-517(1988).
DR   EMBL; X12464; CAA31005.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  885 MW;  33C873333732C72B CRC64;


  Query Match             26.2%;  Score 11;  DB 2;  Length 8;
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  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 LTEKK 5
          |  ||
Db      2 LVLKK 6


RESULT  14
Q9R5L7
ID   Q9R5L7      PRELIMINARY;      PRT;     8 AA.
AC   Q9R5L7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   1,4-BETA-D-GLUCAN GLUCANOHYDROLASE (EC 3.2.1.4) (FRAGMENT).
OS   Clostridium thermocellum.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1515;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92231850; PubMed=1567379;
RA   Romaniec M.P., Fauth U., Kobayashi T., Huskisson N.S., Barker P.J.,
```

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RA   Demain A.L.;
RT   "Purification and characterization of a new endoglucanase from
RT   Clostridium thermocellum.";
RL   Biochem. J. 283:69-73(1992).
SQ   SEQUENCE   8 AA;  823 MW;  C2C1AB1DD9D1B775 CRC64;


  Query Match           26.2%;  Score 11;  DB 2;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 4.7e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      7 SP 8
          ||
Db      1 SP 2


RESULT  15
Q15895
ID   Q15895      PRELIMINARY;      PRT;     8 AA.
AC   Q15895;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   (CLONE XP6A10A) (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA   Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA   Caskey C.T.H.;
RL   Hum. Mol. Genet. 0:0-0(0).
DR   EMBL; L32075; AAA73885.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  921 MW;  C6C735B33686C1AA CRC64;


  Query Match           26.2%;  Score 11;  DB 4;  Length 8;
  Best Local Similarity  50.0%;  Pred. No. 4.7e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 TEKK 5
          |: |
Db      2 TQMK 5


Search completed: December 13, 2001, 12:01:16
Job time: 304 sec
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; Sequence 1, Application US/09424080A
; GENERAL INFORMATION:
;  APPLICANT: ZAVIALOV, Vladimir et al.
;  TITLE OF INVENTION: COMPOSITION FOR ENHANCING IMMUNOSUPPRESANTS PHARMACEUTICAL ACTIVI
;  FILE REFERENCE: 0933-0149P
;  CURRENT APPLICATION NUMBER: US/09/424,080A
;  CURRENT FILING DATE:  2000-02-14
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A peptide corresponding to the high-affinity binding/anti-
;   OTHER INFORMATION: lymphoproliferative
;   OTHER INFORMATION: site of human IFN-alpha
US-09-424-080A-1
LTEKKYSP1
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; Sequence 2, Application US/09424080A
; GENERAL INFORMATION:
;  APPLICANT: ZAVIALOV, Vladimir et al.
;  TITLE OF INVENTION: COMPOSITION FOR ENHANCING IMMUNOSUPPRESANTS PHARMACEUTICAL ACT
;  FILE REFERENCE: 0933-0149P
;  CURRENT APPLICATION NUMBER: US/09/424,080A
;  CURRENT FILING DATE:  2000-02-14
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptides corresponding to the high-affinity binding/anti-
;   OTHER INFORMATION: lymphoproliferative
;   OTHER INFORMATION: site of IFN-alpha, derived from various organisms using sequen
;   OTHER INFORMATION: alignment
;   NAME/KEY: misc_feature
;   LOCATION: (2)..(2)
;   OTHER INFORMATION: Xaa can equal T, R, Q, M, E, or G
;   NAME/KEY: misc_feature
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: Xaa can equal E, R, D, L, I, or A
;   NAME/KEY: misc_feature
;   LOCATION: (4)..(4)
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;   NAME/KEY: misc_feature
;   LOCATION: (5)..(5)
;   OTHER INFORMATION: Xaa can equal K, R, D, N, or S
;   NAME/KEY: misc_feature
;   LOCATION: (6)..(6)
;   OTHER INFORMATION: Xaa can equal Y or H
;   NAME/KEY: misc_feature
;   LOCATION: (7)..(7)
;   OTHER INFORMATION: Xaa can equal  S, R, D, N, or A
;   NAME/KEY: misc_feature
;   LOCATION: (8)..(8)
;   OTHER INFORMATION: Xaa can equal P, R, D, or L
US-09-424-080A-2
LXXXXXXX1
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> O <
O| |O IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "iss" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "new.key":
new (AA) ID new AA preliminary pattern
1 followed by
2 l
2 t or r or q or m or e or g
2 e or r or d or l or i or a
2 k or r or n or m or s or e
2 k or r or d or n or s
2 y or h
2 s or r or d or n or a
2 p or r or d or l

Selected data banks and files:

Data bank : Issued_AA , all entries

-- Output Parameters --

Format Options:		File Options:	
Nucleic acid code matching	Exact	Indirect file	No
Find non-matching hits only	No	Sequence or key file	No
Report key used	Yes	List of hits	Yes
Note position of hit	Yes	Hit display	Yes
Display full annotations	Yes	Name and annotations	Yes
Sequence context	25		

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

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1 match found in sequence:
US-08-669-284B-30 ; Sequence 30, Application US/08669284B
(from "/srch/iaa/5B_COMB.pep")
Sequence 30, Application US/08669284B
Patent No. 5939534
GENERAL INFORMATION:
APPLICANT: Inoue, Makoto
APPLICANT: Kikuchi, Kaoru
APPLICANT: Ishige, Yoko
APPLICANT: Ito, Akira
APPLICANT: Kimura, Toru
APPLICANT: Nakayama, Chikao
APPLICANT: No. 5939534uchi, Hiroshi
TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUROTROPHIC FACTORS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,284B
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/02269
FILING DATE: 27-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 06-268281
FILING DATE: 05-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 06-201504
FILING DATE: 02-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-350934
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-42041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
Found using 'new' (new.key)

|------|
1 LTEKKYSP
1 8

...

-- Search Statistics --

Times:	CPU	Total Elapsed
	00:02:22.04	00:09:53.00

Number of sequences searched:	212306
Number of sequence hits:	124
Number of separate matches:	124
Number of sequence hits saved:	0

GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:45:41 ; Search time 12.78 Seconds
(without alignments)
22.951 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	189	1	INA1_HUMAN	P01562 homo sapien
2	42	100.0	189	1	INA4_HUMAN	P05014 homo sapien
3	42	100.0	189	1	INA5_HUMAN	P01569 homo sapien
4	42	100.0	189	1	INA6_HUMAN	P05013 homo sapien
5	42	100.0	189	1	INAG_HUMAN	P01571 homo sapien
6	42	100.0	189	1	INAK_HUMAN	P01568 homo sapien
7	36	85.7	184	1	INA1_HORSE	P05003 equus cabal
8	36	85.7	184	1	INA2_HORSE	P05004 equus cabal
9	36	85.7	184	1	INA3_HORSE	P05005 equus cabal
10	36	85.7	184	1	INA4_HORSE	P05006 equus cabal
11	36	85.7	188	1	INA2_HUMAN	P01563 homo sapien
12	36	85.7	189	1	INA7_HUMAN	P01567 homo sapien
13	36	85.7	189	1	INAD_HUMAN	P01570 homo sapien
14	36	85.7	194	1	INA_FELCA	P35849 felis silve
15	35	83.3	189	1	INA8_HUMAN	P32881 homo sapien
16	35	83.3	195	1	INO1_HORSE	P05001 equus cabal
17	34	81.0	528	1	LAD1_MOUSE	P57016 mus musculu
18	33	78.6	189	1	INAA_HUMAN	P01566 homo sapien
19	32	76.2	114	1	FVE_FLAVE	P80412 flammulina
20	31	73.8	189	1	INA1_MOUSE	P01572 mus musculu
21	31	73.8	189	1	INA1_PIG	P49879 sus scrofa
22	31	73.8	189	1	INA5_MOUSE	P07349 mus musculu
23	31	73.8	189	1	INA6_MOUSE	P07350 mus musculu
24	31	73.8	189	1	INA8_MOUSE	P17660 mus musculu
25	31	73.8	190	1	INA2_MOUSE	P01573 mus musculu
26	31	73.8	190	1	INA7_MOUSE	P06799 mus musculu
27	31	73.8	190	1	INA9_MOUSE	P09235 mus musculu
28	31	73.8	275	1	BLO3_PSEAE	Q51429 pseudomonas
29	31	73.8	545	1	FLIF_BUCAI	P57175 buchnera ap
30	31	73.8	779	1	ZW10_HUMAN	O43264 homo sapien
31	31	73.8	959	1	N100_YEAST	Q02629 saccharomyc
32	30	71.4	229	1	CSE4_YEAST	P36012 saccharomyc
33	30	71.4	270	1	TPIS_CHLMU	Q9pk66 chlamydia m
34	30	71.4	373	1	Y085_METJA	Q57550 methanococc
35	30	71.4	383	1	COS7_YEAST	Q07788 saccharomyc
36	30	71.4	726	1	NU84_YEAST	P52891 saccharomyc
37	30	71.4	879	1	DPOL_WHV1	P03160 woodchuck h
38	30	71.4	883	1	DPOL_WHV8	P06275 woodchuck h
39	30	71.4	884	1	DPOL_WHV7	P12898 woodchuck h
40	30	71.4	884	1	DPOL_WHV8I	P17396 woodchuck h
41	30	71.4	1294	1	RRPO_WCMVO	P15402 white clove
42	30	71.4	1391	1	RPOB_MYCPN	P78013 mycoplasma
43	29	69.0	189	1	INAF_HUMAN	P05015 homo sapien
44	29	69.0	195	1	INO1_HUMAN	P05000 homo sapien
45	29	69.0	195	1	INO2_HORSE	P05002 equus cabal

ALIGNMENTS

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RESULT 1
INA1_HUMAN
ID   INA1_HUMAN      STANDARD;      PRT;   189 AA.
AC   P01562;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   INTERFERON ALPHA-1/13 PRECURSOR (INTERFERON ALPHA-D) (LEIF D).
GN   IFNA1 AND IFNA13.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81005094; PubMed=6157600;
RA   Mantei N., Schwarzstein M., Streuli M., Panem S., Nagata S.,
RA   Weissmann C.;
RT   "The nucleotide sequence of a cloned human leukocyte interferon
RT   cDNA.";
RL   Gene 10:1-10(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80254543; PubMed=6157095;
RA   Taniguchi T., Mantei N., Schwarzstein M., Nagata S., Muramatsu M.,
RA   Weissmann C.;
RT   "Human leukocyte and fibroblast interferons are structurally
RT   related.";
RL   Nature 285:547-549(1980).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81148795; PubMed=6163083;
RA   Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
RA   McCandliss R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT   "The structure of eight distinct cloned human leukocyte interferon
RT   cDNAs.";
RL   Nature 290:20-26(1981).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85003592; PubMed=6479148;
RA   Todokoro K., Kioussis D., Weissmann C.;
RT   "Two non-allelic human interferon alpha genes with identical coding
RT   regions.";
RL   EMBO J. 3:1809-1812(1984).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- MISCELLANEOUS: INTERFERONS ALPHA-1 AND ALPHA-13 HAVE IDENTICAL
CC       PROTEIN SEQUENCES.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J00210; AAB59403.1; -.
DR   EMBL; V00537; CAA23798.1; -.
DR   EMBL; V00538; CAA23799.1; -.
DR   EMBL; X00803; CAA25381.1; -.
DR   PIR; A01826; IVHUA1.
DR   PIR; C23285; C23285.
DR   HSSP; P01563; 2HIE.
DR   MIM; 147578; -.
DR   MIM; 147660; -.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Multigene family; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    189       INTERFERON ALPHA-1/13.
FT   DISULFID     24    122       BY SIMILARITY.
FT   DISULFID     52    162       BY SIMILARITY.
FT   CONFLICT    137    137       A -> V (IN REF. 3).
SQ   SEQUENCE   189 AA;  21725 MW;  F32F9CB969606B69 CRC64;


  Query Match             100.0%;  Score 42;  DB 1;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    154 LTEKKYSP 161


RESULT   2
INA4_HUMAN
ID   INA4_HUMAN     STANDARD;      PRT;   189 AA.
AC   P05014; P13358;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   INTERFERON ALPHA-4 PRECURSOR (INTERFERON ALPHA-4B) (INTERFERON
DE   ALPHA-M1) (INTERFERON ALPHA-76).
GN   IFNA4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86037205; PubMed=4057246;
RA   Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,
RA   Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
RA   Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT   "Structural relationship of human interferon alpha genes and
RT   pseudogenes.";
RL   J. Mol. Biol. 185:227-260(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84307815; PubMed=6089830;
RA   Linnane A.W., Beilharz M.W., McMullen G.L., Macreadie I.G.,
RA   Murphy M., Nisbet I.T., Novitski C.E., Woodrow G.C.;
RT   "Nucleotide sequence and expression in E. coli of a human interferon-
RT   alpha gene selected from a genomic library using synthetic
RT   oligonucleotides.";
RL   Biochem. Int. 8:725-732(1984).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X02955; CAA26701.1; -.
DR   EMBL; M27318; AAA52726.1; -.
DR   PIR; E23753; IVHU4B.
DR   HSSP; P01563; 1ITF.
DR   MIM; 147564; -.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Multigene family; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    189       INTERFERON ALPHA-4.
FT   DISULFID     24    122       BY SIMILARITY.
FT   DISULFID     52    162       BY SIMILARITY.
FT   CONFLICT     74     74       T -> A (IN REF. 2).
FT   CONFLICT    137    137       V -> E (IN REF. 2).
SQ   SEQUENCE   189 AA;  21808 MW;  4198F9CC8E2AE80C CRC64;


  Query Match             100.0%;  Score 42;  DB 1;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    154 LTEKKYSP 161


RESULT   3
INA5_HUMAN
ID   INA5_HUMAN     STANDARD;      PRT;   189 AA.
AC   P01569;
DT   21-JUL-1986 (Rel. 01, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   INTERFERON ALPHA-5 PRECURSOR (INTERFERON ALPHA-G) (LEIF G) (INTERFERON
DE   ALPHA-61).
GN   IFNA5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86037205; PubMed=4057246;
RA   Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,
RA   Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
RA   Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT   "Structural relationship of human interferon alpha genes and
RT   pseudogenes.";
RL   J. Mol. Biol. 185:227-260(1985).
RN   [2]
RP   SEQUENCE OF 57-189 FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=81148795; PubMed=6163083;
RA   Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
RA   McCandliss R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT   "The structure of eight distinct cloned human leukocyte interferon
RT   cDNAs.";
RL   Nature 290:20-26(1981).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
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CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; X02956; CAA26702.1; -.
DR   EMBL; V00541; CAA23802.1; -.
DR   PIR; A01833; IVHUA7.
DR   HSSP; P01563; 2HIE.
DR   MIM; 147565; -.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Multigene family; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    189       INTERFERON ALPHA-5.
FT   DISULFID     24    122       BY SIMILARITY.
FT   DISULFID     52    162       BY SIMILARITY.
SQ   SEQUENCE   189 AA;  21942 MW;  C605992FE2E78043 CRC64;


  Query Match             100.0%;  Score 42;  DB 1;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db     154 LTEKKYSP 161


RESULT   4
INA6_HUMAN
ID   INA6_HUMAN     STANDARD;      PRT;   189 AA.
AC   P05013;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   INTERFERON ALPHA-6 PRECURSOR (INTERFERON ALPHA-K) (LEIF K) (INTERFERON
DE   ALPHA-54).
GN   IFNA6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86037205; PubMed=4057246;
RA   Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,
RA   Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
RA   Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT   "Structural relationship of human interferon alpha genes and
RT   pseudogenes.";
RL   J. Mol. Biol. 185:227-260(1985).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X02958; CAA26704.1; -.
DR   PIR; A23753; IVHUI6.
DR   HSSP; P01563; 1ITF.
DR   MIM; 147566; -.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Multigene family; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    189       INTERFERON ALPHA-6.
FT   DISULFID     24    122       BY SIMILARITY.
FT   DISULFID     52    162       BY SIMILARITY.
SQ   SEQUENCE   189 AA;  22140 MW;  8C7F3F90F12C562E CRC64;


  Query Match             100.0%;  Score 42;  DB 1;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db     154 LTEKKYSP 161


RESULT   5
INAG_HUMAN
ID   INAG_HUMAN     STANDARD;      PRT;   189 AA.
AC   P01571;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   INTERFERON ALPHA-17 PRECURSOR (INTERFERON ALPHA-I') (INTERFERON
DE   ALPHA-T) (INTERFERON ALPHA-88).
GN   IFNA17.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81201124; PubMed=6165082;
RA   Lawn R.M., Adelman J., Dull T.J., Gross M., Goeddel D.V., Ullrich A.;
RT   "DNA sequence of two closely linked human leukocyte interferon
RT   genes.";
RL   Science 212:1159-1162(1981).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85229953; PubMed=3891272;
RA   Mizoguchi J., Pitha P.M., Raj N.B.K.;
RT   "Efficient expression in Escherichia coli of two species of human
RT   interferon-alpha and their hybrid molecules.";
RL   DNA 4:221-232(1985).
RN   [3]
RP   SEQUENCE OF 14-189 FROM N.A.
RX   MEDLINE=85235859; PubMed=4008999;
RA   Lund B., von Gabain A., Edlund T., Ny T., Lundgren E.;
RT   "Differential expression of interferon genes in a substrain of
RT   Namalwa cells.";
RL   J. Interferon Res. 5:229-238(1985).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; M11026; AAA52725.1; -.
DR   EMBL; V00532; CAA23793.1; -.
DR   EMBL; M71246; AAA52713.1; -.
DR   PIR; A01835; IVHUA9.
DR   PIR; A22255; A22255.
DR   HSSP; P01563; 1ITF.
DR   MIM; 147583; -.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Multigene family; Signal.
FT   SIGNAL       1     23
FT   CHAIN       24    189       INTERFERON ALPHA-17.
FT   DISULFID    24    122       BY SIMILARITY.
FT   DISULFID    52    162       BY SIMILARITY.
FT   CONFLICT    57     57       H -> P (IN REF. 1).
FT   CONFLICT   184    184       I -> R (IN REF. 3).
SQ   SEQUENCE   189 AA;  21728 MW;  0448EAEAB9D7FC32 CRC64;


  Query Match             100.0%;  Score 42;  DB 1;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    154 LTEKKYSP 161


RESULT   6
INAK_HUMAN
ID   INAK_HUMAN     STANDARD;      PRT;   189 AA.
AC   P01568;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   INTERFERON ALPHA-21 PRECURSOR (INTERFERON ALPHA-F) (LEIF F).
GN   IFNA21.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81148795; PubMed=6163083;
RA   Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
RA   McCandliss R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT   "The structure of eight distinct cloned human leukocyte interferon
RT   cDNAs.";
RL   Nature 290:20-26(1981).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Gren E.Y., Berzin V.M., Tsimanis A.Y., Apsalon U.R., Vishnevskii Y.I.,
RA   Yansone I.V., Dishler A.V., Pudova N.V., Smorodintsev A.A.,
RA   Iovlev V.I., Stepanov A.N., Feldmane G.Y., Meldrais Y.A., Lozha V.P.,
RA   Kavsan V.M., Efimov V.A., Sverdlov E.D.;
RT   "A new type of leukocytic interferon.";
RL   Dokl. Biochem. 269:91-95(1983).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
CC   ---------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; M12350; AAA52718.1; -.
DR   EMBL; V00540; CAA23801.1; -.
DR   EMBL; X00145; CAA24980.1; -.
DR   PIR; A01832; IVHUF.
DR   HSSP; P01563; 2HIE.
DR   MIM; 147584; -.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Multigene family; Signal.
FT   SIGNAL       1     23
FT   CHAIN       24    189       INTERFERON ALPHA-21.
FT   DISULFID    24    122       BY SIMILARITY.
FT   DISULFID    52    162       BY SIMILARITY.
FT   CONFLICT   119    119       M -> L (IN REF. 2).
SQ   SEQUENCE   189 AA;  21759 MW;  05B78D86929059B3 CRC64;


  Query Match             100.0%;  Score 42;  DB 1;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    154 LTEKKYSP 161


RESULT   7
INA1_HORSE
ID   INA1_HORSE     STANDARD;      PRT;   184 AA.
AC   P05003;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   01-MAR-1989 (Rel. 10, Last annotation update)
DE   INTERFERON ALPHA-1 PRECURSOR.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87053170; PubMed=3022999;
RA   Himmler A., Hauptmann R., Adolf G.R., Swetly P.;
RT   "Molecular cloning and expression in Escherichia coli of equine type
RT   I interferons.";
RL   DNA 5:345-356(1986).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
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DR   EMBL; M14540; AAA30953.1; -.
DR   PIR; A24912; IVHOA1.
DR   HSSP; P01563; 2HIE.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Multigene family; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    184       INTERFERON ALPHA-1.
FT   DISULFID     24    122       BY SIMILARITY.
FT   DISULFID     52    162       BY SIMILARITY.
SQ   SEQUENCE   184 AA;  20808 MW;  9E860B8CD05C83E6 CRC64;


  Query Match             85.7%;  Score 36;  DB 1;  Length 184;
  Best Local Similarity   87.5%;  Pred. No. 3.6;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           | ||||||
Db     154 LQEKKYSP 161


RESULT   8
INA2_HORSE
ID   INA2_HORSE     STANDARD;      PRT;   184 AA.
AC   P05004;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   01-MAR-1989 (Rel. 10, Last annotation update)
DE   INTERFERON ALPHA-2 PRECURSOR.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87053170; PubMed=3022999;
RA   Himmler A., Hauptmann R., Adolf G.R., Swetly P.;
RT   "Molecular cloning and expression in Escherichia coli of equine type
RT   I interferons.";
RL   DNA 5:345-356(1986).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M14541; AAA30950.1; -.
DR   EMBL; A15987; CAA01258.1; -.
DR   PIR; B24912; IVHOA2.
DR   HSSP; P01563; 2HIE.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Multigene family; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    184       INTERFERON ALPHA-2.
FT   DISULFID     24    122       BY SIMILARITY.
FT   DISULFID     52    162       BY SIMILARITY.
SQ   SEQUENCE   184 AA;  20877 MW;  FC15DC7D811C68EC CRC64;


  Query Match             85.7%;  Score 36;  DB 1;  Length 184;
  Best Local Similarity   87.5%;  Pred. No. 3.6;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           | ||||||
Db     154 LQEKKYSP 161


RESULT   9
INA3_HORSE
ID   INA3_HORSE     STANDARD;      PRT;   184 AA.
AC   P05005;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   01-MAR-1989 (Rel. 10, Last annotation update)
DE   INTERFERON ALPHA-3 PRECURSOR.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87053170; PubMed=3022999;
RA   Himmler A., Hauptmann R., Adolf G.R., Swetly P.;
RT   "Molecular cloning and expression in Escherichia coli of equine type
RT   I interferons.";
RL   DNA 5:345-356(1986).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M14542; AAA30951.1; -.
DR   EMBL; A16555; CAA01292.1; -.
DR   PIR; C24912; IVHOA3.
DR   HSSP; P01563; 2HIE.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Multigene family; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    184       INTERFERON ALPHA-3.
FT   DISULFID     24    122       BY SIMILARITY.
FT   DISULFID     52    162       BY SIMILARITY.
SQ   SEQUENCE   184 AA;  20782 MW;  4C15D991ECA6D24A CRC64;


  Query Match             85.7%;  Score 36;  DB 1;  Length 184;
  Best Local Similarity   87.5%;  Pred. No. 3.6;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           | ||||||
Db     154 LQEKKYSP 161
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RESULT  10
INA4_HORSE
ID   INA4_HORSE     STANDARD;      PRT;   184 AA.
AC   P05006;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   01-MAR-1989 (Rel. 10, Last annotation update)
DE   INTERFERON ALPHA-4 PRECURSOR.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87053170; PubMed=3022999;
RA   Himmler A., Hauptmann R., Adolf G.R., Swetly P.;
RT   "Molecular cloning and expression in Escherichia coli of equine type
RT   I interferons.";
RL   DNA 5:345-356(1986).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; M14543; AAA30952.1; -.
DR   PIR; D24912; IVHOA4.
DR   HSSP; P01563; 1ITF.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Multigene family; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    184       INTERFERON ALPHA-4.
FT   DISULFID     24    122       BY SIMILARITY.
FT   DISULFID     52    162       BY SIMILARITY.
SQ   SEQUENCE   184 AA;  20860 MW;  FC087F46F11C68EC CRC64;


  Query Match             85.7%;  Score 36;  DB 1;  Length 184;
  Best Local Similarity   87.5%;  Pred. No. 3.6;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           | ||||||
Db     154 LQEKKYSP 161


RESULT  11
INA2_HUMAN
ID   INA2_HUMAN     STANDARD;      PRT;   188 AA.
AC   P01563; P01564; Q14606;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   INTERFERON ALPHA-2 PRECURSOR (INTERFERON ALPHA-A) (LEIF A).
GN   IFNA2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81052322; PubMed=6159538;
RA   Goeddel D.V., Yelverton E., Ullrich A., Heyneker H.L., Miozzari G.,
RA   Holmes W., Seeburg P.H., Dull T.J., May L., Stebbing N., Crea R.,
RA   Maeda S., McCandliss R., Sloma A., Tabor J.M., Gross M.,
RA   Familletti P.C., Pestka S.;
RT   "Human leukocyte interferon produced by E. coli is biologically
RT   active.";
RL   Nature 287:411-416(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81148795; PubMed=6163083;
RA   Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
RA   McCandliss R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT   "The structure of eight distinct cloned human leukocyte interferon
RT   cDNAs.";
RL   Nature 290:20-26(1981).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82060261; PubMed=6170983;
RA   Lawn R.M., Gross M., Houck C.M., Franke A.E., Gray P.V.,
RA   Goeddel D.V.;
RT   "DNA sequence of a major human leukocyte interferon gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:5435-5439(1981).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow tumor;
RX   MEDLINE=86069501; PubMed=3906813;
RA   Oliver G., Balbas P., Valle F., Soberon X., Bolivar F.;
RT   "Cloning of human leukocyte interferon cDNA and a strategy for its
RT   production in E. coli.";
RL   Rev. Latinoam. Microbiol. 27:141-150(1985).
RN   [5]
RP   SEQUENCE OF 7-188 FROM N.A.
RX   MEDLINE=81015442; PubMed=6158094;
RA   Streuli M., Nagata S., Weissmann C.;
RT   "At least three human type alpha interferons: structure of alpha 2.";
RL   Science 209:1343-1347(1980).
RN   [6]
RP   SEQUENCE OF 24-188 FROM N.A.
RX   MEDLINE=83299241; PubMed=6310510;
RA   Weber H., Weissmann C.;
RT   "Formation of genes coding for hybrid proteins by recombination
RT   between related, cloned genes in E. coli.";
RL   Nucleic Acids Res. 11:5661-5669(1983).
RN   [7]
RP   SEQUENCE OF 24-112 AND 136-188.
RX   MEDLINE=81052321; PubMed=6159537;
RA   Allen G., Fantes K.H.;
RT   "A family of structural genes for human lymphoblastoid
RT   (leukocyte-type) interferon.";
RL   Nature 287:408-411(1980).
RN   [8]
RP   DISULFIDE BONDS.
RX   MEDLINE=81123083; PubMed=6162107;
RA   Wetzel R.;
RT   "Assignment of the disulphide bonds of leukocyte interferon.";
RL   Nature 289:606-607(1981).
RN   [9]
RP   CARBOHYDRATE-LINKAGE SITE THR-129.
RX   MEDLINE=91264809; PubMed=2049076;
RA   Adolf G.R., Kalsner I., Ahorn H., Maurer Fogy I., Cantell K.;
RT   "Natural human interferon-alpha 2 is O-glycosylated.";
RL   Biochem. J. 276:511-518(1991).
RN   [10]
RP   3D-STRUCTURE MODELING.
RX   MEDLINE=94052087; PubMed=8234245;
RA   Murgolo N.J., Windsor W.T., Hruza A., Reichert P., Tsarbopoulos A.,
RA   Baldwin S., Huang E., Pramanik B., Ealick S., Trotta P.P.;
RT   "A homology model of human interferon alpha-2.";
RL   Proteins 17:62-74(1993).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
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RX   MEDLINE=97148339; PubMed=8994971;
RA   Radhakrishnan R., Walter L.J., Hruza A., Reichert P., Trotta P.P.,
RA   Nagabhushan T.L., Walter M.R.;
RT   "Zinc mediated dimer of human interferon-alpha 2b revealed by X-ray
RT   crystallography.";
RL   Structure 4:1453-1463(1996).
RN   [12]
RP   STRUCTURE BY NMR.
RX   MEDLINE=98118493; PubMed=9417943;
RA   Klaus W., Gsell B., Labhardt A.M., Wipf B., Senn H.;
RT   "The three-dimensional high resolution structure of human interferon
RT   alpha-2a determined by heteronuclear NMR spectroscopy in solution.";
RL   J. Mol. Biol. 274:661-675(1997).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- POLYMORPHISM: TWO FORMS, ALPHA-2A AND ALPHA-2B DIFFER BY A SINGLE
CC       RESIDUE (POSITION 46).
CC   -!- PHARMACEUTICAL: AVAILABLE UNDER THE NAMES ROFERON-A (ROCHE) OR
CC       INTRON-A (SCHERING-PLOUGH). USED AS AN ANTICANCER DRUG FOR ITS
CC       ANTIPROLIFERATIVE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; J00207; AAB59402.1; -.
DR   EMBL; V00544; CAA23805.1; -.
DR   EMBL; V00548; CAA23809.1; -.
DR   EMBL; V00549; CAA23810.1; -.
DR   EMBL; M54886; AAA59181.1; -.
DR   EMBL; M29883; AAA52715.1; -.
DR   EMBL; A04970; CAA00410.1; -.
DR   PIR; A01827; IVHUA2.
DR   PIR; A01828; IVHUA3.
DR   PDB; 2HIE; 31-AUG-94.
DR   PDB; 1RH2; 12-NOV-97.
DR   PDB; 1ITF; 03-DEC-97.
DR   GlycoSuiteDB; P01563; -.
DR   MIM; 147562; -.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Multigene family; Signal; Glycoprotein;
KW   Polymorphism; Pharmaceutical; 3D-structure.
FT   SIGNAL        1     23
FT   CHAIN        24    188       INTERFERON ALPHA-2.
FT   DISULFID     24    121
FT   DISULFID     52    161
FT   CARBOHYD    129    129       O-LINKED (GALNAC. . .).
FT                                 /FTId=CAR_000049.
FT   VARIANT      46     46       K -> R (IN ALPHA-2B).
FT                                 /FTId=VAR_004012.
SQ   SEQUENCE   188 AA;  21550 MW;  101DD21D394CBF97 CRC64;
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  Query Match             85.7%;  Score 36;  DB 1;  Length 188;
  Best Local Similarity   87.5%;  Pred. No. 3.7;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            | ||||||
Db     153 LKEKKYSP 160
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RESULT  12
INA7_HUMAN
ID   INA7_HUMAN     STANDARD;      PRT;   189 AA.
AC   P01567;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   INTERFERON ALPHA-7 PRECURSOR (INTERFERON ALPHA-J1) (INTERFERON
DE   ALPHA-J) (LEIF J).
GN   IFNA7.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86037205; PubMed=4057246;
RA   Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,
RA   Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
RA   Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT   "Structural relationship of human interferon alpha genes and
RT   pseudogenes.";
RL   J. Mol. Biol. 185:227-260(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83010248; PubMed=6181262;
RA   Ullrich A., Gray A., Goeddel D.V., Dull T.J.;
RT   "Nucleotide sequence of a portion of human chromosome 9 containing a
RT   leukocyte interferon gene cluster.";
RL   J. Mol. Biol. 156:467-486(1982).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V00531; CAA23792.1; -.
DR   EMBL; X02960; CAA26706.1; -.
DR   PIR; A01831; IVHUA0.
DR   HSSP; P01563; 2HIE.
DR   MIM; 147567; -.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Multigene family; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    189       INTERFERON ALPHA-7.
FT   DISULFID     24    122       BY SIMILARITY.
FT   DISULFID     52    162       BY SIMILARITY.
SQ   SEQUENCE   189 AA;  22106 MW;  9DF6F5C81E339A42 CRC64;
```

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  Query Match             85.7%;  Score 36;  DB 1;  Length 189;
  Best Local Similarity   87.5%;  Pred. No. 3.7;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            | ||||||
Db     154 LMEKKYSP 161
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RESULT  13
INAD_HUMAN
ID   INAD_HUMAN     STANDARD;      PRT;   189 AA.
AC   P01570;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   INTERFERON ALPHA-14 PRECURSOR (INTERFERON ALPHA-H) (LEIF H)
DE   (INTERFERON LAMBDA-2-H).
GN   IFNA14.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86037205; PubMed=4057246;
RA   Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,
RA   Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
RA   Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT   "Structural relationship of human interferon alpha genes and
RT   pseudogenes.";
RL   J. Mol. Biol. 185:227-260(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81201124; PubMed=6165082;
RA   Lawn R.M., Adelman J., Dull T.J., Gross M., Goeddel D.V., Ullrich A.;
RT   "DNA sequence of two closely linked human leukocyte interferon
RT   genes.";
RL   Science 212:1159-1162(1981).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81148795; PubMed=6163083;
RA   Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
RA   McCandliss R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT   "The structure of eight distinct cloned human leukocyte interferon
RT   cDNAs.";
RL   Nature 290:20-26(1981).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- MISCELLANEOUS: A VARIANT SEQUENCE DIFFERS IN 3 POSITIONS. THE LAST
CC       2 BEING THE RESULT OF A DELETION FOLLOWED BY AN INSERTION.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V00533; CAA23794.1; -.
DR   EMBL; X02959; CAA26705.1; -.
DR   EMBL; V00542; CAA23803.1; -.
DR   PIR; C23753; IVHU14.
DR   HSSP; P01563; 2HIE.
DR   MIM; 147579; -.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Multigene family; Glycoprotein; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    189       INTERFERON ALPHA-14.
FT   DISULFID     24    122       BY SIMILARITY.
FT   DISULFID     52    162       BY SIMILARITY.
FT   CARBOHYD     25     25       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     175    175       L -> F.
FT                                /FTId=VAR_004013.
FT   VARIANT     182    182       Q -> K.
FT                                /FTId=VAR_004014.
FT   VARIANT     184    184       R -> G.
FT                                /FTId=VAR_004015.
SQ   SEQUENCE   189 AA;  22062 MW;  B6B71E2F0D644FE7 CRC64;


  Query Match          85.7%;  Score 36;  DB 1;  Length 189;
  Best Local Similarity   87.5%;  Pred. No. 3.7;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           | ||||||
Db     154 LMEKKYSP 161


RESULT  14
INA_FELCA
ID   INA_FELCA      STANDARD;      PRT;   194 AA.
AC   P35849; Q28831;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   INTERFERON ALPHA PRECURSOR (IFN-ALPHA).
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92323151; PubMed=1377975;
RA   Nakamura N., Sudo T., Matsuda S., Yanai A.;
RT   "Molecular cloning of feline interferon cDNA by direct expression.";
RL   Biosci. Biotechnol. Biochem. 56:211-214(1992).
RN   [2]
RP   SEQUENCE OF 1-193 FROM N.A.
RX   MEDLINE=93291263; PubMed=7685640;
RA   Ueda Y., Sakurai T., Yanai A.;
RT   "Homogeneous production of feline interferon in silkworm by replacing
RT   single amino acid code in signal peptide region in recombinant
RT   baculovirus and characterization of the product.";
RL   J. Vet. Med. Sci. 55:251-258(1993).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S62636; AAB27160.2; -.
DR   PIR; JS0664; JS0664.
DR   HSSP; P01563; 2HIE.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Signal.
FT   SIGNAL        1     23       BY SIMILARITY.
FT   CHAIN        24    194       INTERFERON ALPHA.
FT   DISULFID     24    123       BY SIMILARITY.
FT   DISULFID     52    166       BY SIMILARITY.
FT   CARBOHYD    102    102       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     21     21       S -> V (IN REF. 2).
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SQ   SEQUENCE   194 AA;  21892 MW;  D10E916E3755BFEF CRC64;


  Query Match             85.7%;  Score 36;  DB 1;  Length 194;
  Best Local Similarity   87.5%;  Pred. No. 3.8;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           | ||||||
Db     158 LQEKKYSP 165


RESULT  15
INA8_HUMAN
ID   INA8_HUMAN     STANDARD;      PRT;   189 AA.
AC   P32881; P09236; P01565;
DT   21-JUL-1986 (Rel. 01, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   INTERFERON ALPHA-8 PRECURSOR (INTERFERON ALPHA-B2) (INTERFERON
DE   ALPHA-B) (LEIF B).
GN   IFNA8.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86037205; PubMed=4057246;
RA   Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,
RA   Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
RA   Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT   "Structural relationship of human interferon alpha genes and
RT   pseudogenes.";
RL   J. Mol. Biol. 185:227-260(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84183614; PubMed=6325303;
RA   Bowden D.W., Mao J., Gill T., Hsiao K., Lillquist J.S., Testa D.,
RA   Vovis G.F.;
RT   "Cloning of eukaryotic genes in single-strand phage vectors: the
RT   human interferon genes.";
RL   Gene 27:87-99(1984).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81174733; PubMed=6164048;
RA   Yelverton E., Leung D., Weck P., Gray P.W., Goeddel D.V.;
RT   "Bacterial synthesis of a novel human leukocyte interferon.";
RL   Nucleic Acids Res. 9:731-741(1981).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81148795; PubMed=6163083;
RA   Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
RA   McCandliss R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
RT   "The structure of eight distinct cloned human leukocyte interferon
RT   cDNAs.";
RL   Nature 290:20-26(1981).
CC   -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC       ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC       A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V00545; CAA23806.1; -.
DR   EMBL; K01900; AAA52716.1; -.
DR   EMBL; X03125; CAA26903.1; -.
DR   EMBL; V00550; CAA23811.1; -.
DR   PIR; D23753; IVHUI8.
DR   PIR; A01829; IVHUA4.
DR   HSSP; P01563; 2HIE.
DR   MIM; 147568; -.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Cytokine; Antiviral; Multigene family; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    189       INTERFERON ALPHA-8.
FT   DISULFID     24    122       BY SIMILARITY.
FT   DISULFID     52    162       BY SIMILARITY.
FT   CONFLICT      8      8       L -> M (IN REF. 3 AND 4).
FT   CONFLICT    121    124       SCVM -> VLCD (IN REF. 3 AND 4).
SQ   SEQUENCE   189 AA;  21989 MW;  83128DA2B6DBB2C1 CRC64;


  Query Match             83.3%;  Score 35;  DB 1;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYS 7
           |||||||
Db     154 LTEKKYS 160


Search completed: December 13, 2001, 10:50:49
Job time: 308 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:45:11 ; Search time 35.74 Seconds
(without alignments)
32.741 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	166	4	Q9UMJ3	Q9umj3 homo sapien
2	42	100.0	181	4	Q14608	Q14608 homo sapien
3	42	100.0	189	4	Q14605	Q14605 homo sapien
4	42	100.0	189	4	Q14639	Q14639 homo sapien
5	42	100.0	189	4	Q14607	Q14607 homo sapien
6	36	85.7	108	6	Q9N1U6	Q9n1u6 equus cabal
7	36	85.7	170	6	Q29114	Q29114 sus scrofa
8	36	85.7	170	6	Q29115	Q29115 sus scrofa
9	36	85.7	730	10	Q9S9M5	Q9s9m5 arabidopsis
10	34	81.0	181	3	O13619	O13619 schizosacch
11	34	81.0	577	5	O35995	O35995 vairimorpha
12	34	81.0	1154	5	Q9V6S9	Q9v6s9 drosophila
13	33	78.6	110	10	Q9SYY5	Q9syy5 arabidopsis
14	33	78.6	334	2	Q9CKT2	Q9ckt2 pasteurella
15	33	78.6	767	11	Q9WTU7	Q9wtu7 mus musculu
16	32	76.2	83	5	Q9V8W6	Q9v8w6 drosophila
17	32	76.2	400	5	Q9VBY9	Q9vby9 drosophila
18	32	76.2	414	10	Q9SX74	Q9sx74 arabidopsis
19	32	76.2	573	5	Q23323	Q23323 caenorhabdi
20	32	76.2	1528	5	Q95022	Q95022 cryptospori
21	31	73.8	60	12	Q9IEU9	Q9ieu9 cotton leaf
22	31	73.8	113	2	Q9F554	Q9f554 escherichia
23	31	73.8	118	12	Q88551	Q88551 tomato yell
24	31	73.8	118	12	O73583	O73583 cotton leaf
25	31	73.8	118	12	Q9QDE8	Q9qde8 tomato leaf
26	31	73.8	118	12	Q9IGY3	Q9igy3 tobacco lea
27	31	73.8	118	12	Q9IGX7	Q9igx7 tobacco gem
28	31	73.8	118	12	Q99DR5	Q99dr5 chilli leaf
29	31	73.8	136	11	Q61717	Q61717 mus musculu
30	31	73.8	176	11	Q9D380	Q9d380 mus musculu
31	31	73.8	190	11	Q61716	Q61716 mus musculu
32	31	73.8	190	11	Q61718	Q61718 mus musculu
33	31	73.8	190	11	Q61719	Q61719 mus musculu
34	31	73.8	197	2	O06983	O06983 bacillus su
35	31	73.8	199	4	Q9Y6W8	Q9y6w8 homo sapien
36	31	73.8	201	2	Q45137	Q45137 bacteroides
37	31	73.8	239	2	Q9Z4D2	Q9z4d2 escherichia
38	31	73.8	261	2	P96679	P96679 bacillus su
39	31	73.8	275	2	P94124	P94124 acinetobact
40	31	73.8	285	3	Q00875	Q00875 fusarium so
41	31	73.8	322	4	Q92780	Q92780 homo sapien
42	31	73.8	401	1	O59114	O59114 pyrococcus
43	31	73.8	439	2	Q9RGV4	Q9rgv4 salmonella
44	31	73.8	510	2	Q9RK66	Q9rk66 streptomyce
45	31	73.8	589	2	Q9RMV4	Q9rmv4 bacillus an

ALIGNMENTS

RESULT 1
Q9UMJ3
ID Q9UMJ3 PRELIMINARY; PRT; 166 AA.
AC Q9UMJ3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE IFNA PROTEIN (FRAGMENT).
GN IFNA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83299241; PubMed=6310510;
RA Weber H., Weissmann C.;
RT "Formation of genes coding for hybrid proteins by recombination
RT between related, cloned genes in E. coli.";
RL Nucleic Acids Res. 11:5661-5669(1983).
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
DR EMBL; M29884; AAA52714.1; -.
DR HSSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
FT NON_TER 1 1
SQ SEQUENCE 166 AA; 19386 MW; 4152EA2A78361BB8 CRC64;

Query Match 100.0%; Score 42; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 131 LTEKKYSP 138

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RESULT   2
Q14608
ID   Q14608      PRELIMINARY;      PRT;   181 AA.
AC   Q14608;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   LEUKOCYTE INTERFERON-ALPHA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85056523; PubMed=6548765;
RA   Gren E., Berzin V.M., Jansone I., Tsimanis A., Vishnevsky Y.,
RA   Apsalons U.;
RT   "Novel human leukocyte interferon subtype and structural comparison of
RT   alpha interferon genes.";
RL   J. Interferon Res. 4:609-617(1984).
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
DR   EMBL; M28586; AAA36041.1; -.
DR   HSSP; P01563; 2HIE.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral; Cytokine; Signal.
SQ   SEQUENCE   181 AA;  20878 MW;  3DB45120764EBABC CRC64;


  Query Match             100.0%;  Score 42;  DB 4;  Length 181;
  Best Local Similarity   100.0%;  Pred. No. 0.71;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    146 LTEKKYSP 153


RESULT   3
Q14605
ID   Q14605      PRELIMINARY;      PRT;   189 AA.
AC   Q14605;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   INTERFERON-ALPHA 13 PRECURSOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Rostoks N.;
RL   Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86037205; PubMed=4057246;
RA   Henco K., Brosius J., Fujisawa A., Fujisawa J.I., Haynes J.R.,
RA   Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
RA   Todokoro K., Waelchli M., Nagata S., Weissmann C.;
RT   "Structural relationship of human interferon alpha genes and
RT   pseudogenes.";
RL   J. Mol. Biol. 185:227-260(1985).
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
DR   EMBL; X75934; CAA53538.1; -.
DR   EMBL; A07163; CAA00632.1; -.
DR   HSSP; P01563; 2HIE.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral; Cytokine; Signal.
FT   SIGNAL       1     23       POTENTIAL.
FT   CHAIN       24    189       POTENTIAL.
SQ   SEQUENCE   189 AA;  21697 MW;  442F8BB754D88398 CRC64;


  Query Match             100.0%;  Score 42;  DB 4;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.74;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    154 LTEKKYSP 161


RESULT   4
Q14639
ID   Q14639      PRELIMINARY;      PRT;   189 AA.
AC   Q14639;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   LEUCOCYTE INTERFERON PRECURSOR.
GN   IFNA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87024453; PubMed=3767336;
RA   Saveliev V.I., Zlochevsky M.L., Sorokin A.V., Naroditskaya V.A.,
RA   Bolotin A.P., Demyanova N.G., Kozlov Y.I., Neznanov N.S.,
RA   Gazaryan K.G., Monastyrskaya G.S., Sverdlov E.D.;
RT   "[Cloning and the determination of the nucleotide sequences in 2 genes
RT   of human leukocyte interferons].";
RL   Antibiot. Med. Biotekhnol. 31:592-596(1986).
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
DR   EMBL; M38289; AAA59165.1; -.
DR   HSSP; P01563; 2HIE.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral; Cytokine; Signal.
FT   SIGNAL       1     23       POTENTIAL.
FT   CHAIN       24    189       POTENTIAL.
SQ   SEQUENCE   189 AA;  21781 MW;  9D6E31870F1A88A1 CRC64;


  Query Match             100.0%;  Score 42;  DB 4;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.74;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    154 LTEKKYSP 161


RESULT   5
Q14607
ID   Q14607      PRELIMINARY;      PRT;   189 AA.
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AC   Q14607;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   INTERFERON-ALPHA-J1 (IFN-ALPHA-J1).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86005847; PubMed=2995168;
RA   Cohen S., Velan B., Grosfeld H., Shalita Z., Leitner M.,
RA   Shafferman A.;
RT   "Cloning, expression and biological activity of a new variant of human
RT   interferon alpha identified in virus induced lymphoblastoid cells.";
RL   Dev. Biol. 60:111-122(1985).
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
DR   EMBL; M34913; AAA36039.1; -.
DR   HSSP; P01563; 2HIE.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral; Cytokine.
SQ   SEQUENCE   189 AA;  22048 MW;  2AF6F48447BB72B3 CRC64;


  Query Match             100.0%;  Score 42;  DB 4;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 0.74;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
Db     154 LTEKKYSP 161


RESULT   6
Q9N1U6
ID   Q9N1U6      PRELIMINARY;      PRT;   108 AA.
AC   Q9N1U6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   INTERFERON ALPHA-1 (FRAGMENT).
GN   IFN1A.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20082971; PubMed=10613847;
RA   Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA   Bowling A.T., Murray J.D.;
RT   "A comparative gene map of the horse (Equus caballus).";
RL   Genome Res. 9:1239-1249(1999).
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
DR   EMBL; AF135017; AAF29603.1; -.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral; Cytokine.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  12420 MW;  028CA54FFA97F4CD CRC64;


  Query Match             85.7%;  Score 36;  DB 6;  Length 108;
  Best Local Similarity   87.5%;  Pred. No. 7.1;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           | ||||||
Db      95 LQEKKYSP 102


RESULT   7
Q29114
ID   Q29114      PRELIMINARY;      PRT;   170 AA.
AC   Q29114;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SHORT TYPE I INTERFERON PRECURSOR.
GN   SPI IFN.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=WHOLE CONCEPTUS (EMBRYO PLUS TROPHOBLAST);
RX   MEDLINE=93374975; PubMed=7690039;
RA   Lefevre F., Boulay V.;
RT   "A novel and atypical type one interferon gene expressed by
RT   trophoblast during early pregnancy.";
RL   J. Biol. Chem. 268:19760-19768(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=WHOLE CONCEPTUS (EMBRYO PLUS TROPHOBLAST);
RX   MEDLINE=86232600; PubMed=3714490;
RA   von Heijne G.;
RT   "A new method for predicting signal sequence cleavage sites.";
RL   Nucleic Acids Res. 14:4683-4690(1986).
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
DR   EMBL; Z22706; CAA80407.1; -.
DR   HSSP; P01563; 1ITF.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral; Cytokine; Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    170       SHORT TYPE I INTERFERON.
FT   VARIANT      88     88       S -> G.
FT   VARIANT     101    101       N -> T.
SQ   SEQUENCE   170 AA;  19906 MW;  FED195EAFDD99AAB CRC64;


  Query Match             85.7%;  Score 36;  DB 6;  Length 170;
  Best Local Similarity   87.5%;  Pred. No. 11;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           | ||||||
Db     146 LKEKKYSP 153


RESULT   8
Q29115
ID   Q29115      PRELIMINARY;      PRT;   170 AA.
AC   Q29115;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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DE   SHORT TYPE I INTERFERON PRECURSOR.
GN   SPI IFN.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LARGE WHITE BREED; TISSUE=LIVER;
RX   MEDLINE=86232600; PubMed=3714490;
RA   von Heijne G.;
RT   "A new method for predicting signal sequence cleavage sites.";
RL   Nucleic Acids Res. 14:4683-4690(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LARGE WHITE BREED; TISSUE=LIVER;
RX   MEDLINE=87174805; PubMed=3550702;
RA   Singer D.S., Parent L.J., Ehrlich R.;
RT   "Identification and DNA sequence of an interspersed repetitive DNA
RT   element in the genome of the miniature swine.";
RL   Nucleic Acids Res. 15:2780-2780(1987).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LARGE WHITE BREED; TISSUE=LIVER;
RX   MEDLINE=93374975; PubMed=7690039;
RA   Lefevre F., Boulay V.;
RT   "A novel and atypical type one interferon gene expressed by
RT   trophoblast during early pregnancy.";
RL   J. Biol. Chem. 268:19760-19768(1993).
CC   -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC       FAMILY.
DR   EMBL; Z22707; CAA80408.1; -.
DR   HSSP; P01563; 1ITF.
DR   InterPro; IPR000471; Interferon_abd.
DR   Pfam; PF00143; interferon; 1.
DR   PRINTS; PR00266; INTERFERONAB.
DR   ProDom; PD000550; Interferon_abd; 1.
DR   SMART; SM00076; IFabd; 1.
DR   PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW   Antiviral; Cytokine; Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    170       SHORT TYPE I INTERFERON.
SQ   SEQUENCE   170 AA;  19863 MW;  563F7D2AE716AF51 CRC64;


  Query Match             85.7%;  Score 36;  DB 6;  Length 170;
  Best Local Similarity   87.5%;  Pred. No. 11;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            | ||||||
Db     146 LKEKKYSP 153


RESULT   9
Q9S9M5
ID   Q9S9M5      PRELIMINARY;      PRT;   730 AA.
AC   Q9S9M5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   T24D18.20 PROTEIN.
GN   T24D18.20.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Liu S.X., Yu G., Sakano H., Jhaveri A., Lee J.M., Lenz C., Pham P.,
RA   Toriumi M., Chin C., Chiou J., Choi E., Chung M., Gonzalez A.,
RA   Howng B., Koo T., Li J., Liu A., Vaysberg M., Altafi H., Brooks S.,
RA   Buehler E., Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C.,
RA   Khan S., Kim C., Lam B., Nguyen M., Palm C., Shinn P., Tambunga G.,
RA   Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT   "The sequence of BAC T24D18 from Arabidopsis thaliana chromosome 1.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Theologis A.;
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Theologis;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR   EMBL; AC010924; AAF18507.1; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_kin_actsite.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00221; STYKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   730 AA;  81210 MW;  B51DB48D995C73B5 CRC64;


  Query Match             85.7%;  Score 36;  DB 10;  Length 730;
  Best Local Similarity   75.0%;  Pred. No. 45;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||:|:|||
Db     224 LTDKRYSP 231


RESULT  10
O13619
ID   O13619      PRELIMINARY;      PRT;   181 AA.
AC   O13619;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PI028 PROTEIN (HYPOTHETICAL 20.3 KDA PROTEIN).
GN   PI028 OR SPBP22H7.03.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972 H-;
RA   Kushida N., Yamazaki S., Tanaka T., Jinno K., Haikawa Y., Yamazaki J.,
RA   Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K.,
RA   Ogura K., Otsuka R., Kudoh Y., Yanagida M., Machida M., Zhang M.Q.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972H-;
RA   Murphy L., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB004535; BAA21407.1; -.
DR   EMBL; AL590883; CAC37371.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   181 AA;  20293 MW;  2D6A1B61F0FD51E8 CRC64;


  Query Match             81.0%;  Score 34;  DB 3;  Length 181;
  Best Local Similarity   85.7%;  Pred. No. 30;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      2 TEKKYSP 8
          :||||||
Db     70 SEKKYSP 76


RESULT  11
O35995
ID   O35995      PRELIMINARY;      PRT;   577 AA.
AC   O35995;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MITOCHONDRIAL HSP70 HOMOLOG.
OS   Vairimorpha necatrix.
OC   Eukaryota; Microsporidia; Burenellidae; Vairimorpha.
OX   NCBI_TaxID=6039;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPORES;
RA   Hirt R.P., Healy B., Vossbrinck C.R., Canning E.U., Embley T.M.;
RL   Curr. Biol. 7:0-0(1997).
DR   EMBL; AF008215; AAB81494.1; -.
DR   InterPro; IPR001023; HSP70.
DR   Pfam; PF00012; HSP70; 1.
DR   PROSITE; PS00297; HSP70_1; 1.
DR   PROSITE; PS00329; HSP70_2; 1.
SQ   SEQUENCE   577 AA;  64744 MW;  C649B069A94D0D8B CRC64;


  Query Match             81.0%;  Score 34;  DB 5;  Length 577;
  Best Local Similarity   75.0%;  Pred. No. 91;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          : ||||||
Db    110 IDEKKYSP 117


RESULT  12
Q9V6S9
ID   Q9V6S9      PRELIMINARY;      PRT;  1154 AA.
AC   Q9V6S9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   CG18368 PROTEIN.
GN   CG18368.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003817; AAF58343.1; -.
DR   FlyBase; FBgn0033864; CG18368.
SQ   SEQUENCE   1154 AA;  134414 MW;  A1985DEF780A01BA CRC64;


  Query Match             81.0%;  Score 34;  DB 5;  Length 1154;
  Best Local Similarity   85.7%;  Pred. No. 1.8e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TEKKYSP 8
          |:|||||
Db    166 TKKKYSP 172


RESULT  13
Q9SYY5
ID   Q9SYY5      PRELIMINARY;      PRT;   110 AA.
AC   Q9SYY5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   HYPOTHETICAL 13.2 KDA PROTEIN.
GN   C7A10.800 OR AT4G36560.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bevan M., Terryn N., Vos P., Heijnen L., Mewes H.W., Mayer K.F.X.,
RA   Schueller C.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z99708; CAB16837.1; -.
DR   EMBL; AL161589; CAB80322.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   110 AA;  13189 MW;  82DA67BF97311BA8 CRC64;


  Query Match             78.6%;  Score 33;  DB 10;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 EKKYSP 8
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          ||||||
Db     36 EKKYSP 41


RESULT  14
Q9CKT2
ID   Q9CKT2      PRELIMINARY;      PRT;   334 AA.
AC   Q9CKT2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   HPAA.
GN   HPAA OR PM1524.
OS   Pasteurella multocida.
OC   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC   Pasteurella.
OX   NCBI_TaxID=747;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PM70;
RX   MEDLINE=21145866; PubMed=11248100;
RA   May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT   "Complete genomic sequence of Pasteurella multocida Pm70.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC   -!- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
CC       REGULATORS.
DR   EMBL; AE006189; AAK03608.1; -.
DR   InterPro; IPR000005; HTHAraC.
DR   Pfam; PF00165; HTH_AraC; 1.
DR   PRINTS; PR00032; HTHARAC.
DR   SMART; SM00342; HTH_ARAC; 1.
DR   PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR   PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW   Complete proteome; DNA-binding; Transcription regulation.
SQ   SEQUENCE   334 AA;  39714 MW;  8532929C52246503 CRC64;


  Query Match           78.6%;  Score 33;  DB 2;  Length 334;
  Best Local Similarity  100.0%;  Pred. No. 85;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 EKKYSP 8
          ||||||
Db    214 EKKYSP 219


RESULT  15
Q9WTU7
ID   Q9WTU7      PRELIMINARY;      PRT;   767 AA.
AC   Q9WTU7;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   APOPTOSIS-LINKED PROTEIN 4, DELTAC FORM (FRAGMENT).
GN   PDCD11 OR ALG-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99244237; PubMed=10229231;
RA   Lacana' E., D'Adamio L.;
RT   "Regulation of fas ligand expression and cell death by apoptosis-
RT   linked gene 4.";
RL   Nat. Med. 5:542-547(1999).
DR   EMBL; AF055668; AAD20941.1; -.
DR   HSSP; P05055; 1SRO.
DR   MGD; MGI:1341788; Pdcd11.
DR   InterPro; IPR000110; Ribosomal_S1.
DR   InterPro; IPR003029; S1.
DR   Pfam; PF00575; S1; 4.
DR   PRINTS; PR00681; RIBOSOMALS1.
DR   SMART; SM00316; S1; 6.
FT   NON_TER       1       1
FT   NON_TER     767     767
SQ   SEQUENCE   767 AA;  84512 MW;  81B692B073E697FA CRC64;


  Query Match           78.6%;  Score 33;  DB 11;  Length 767;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 EKKYSP 8
          ||||||
Db    101 EKKYSP 106


Search completed: December 13, 2001, 10:50:30
Job time: 319 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:44:40 ; Search time 38.61 Seconds
(without alignments)
15.348 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101:*
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2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	11	15	AAR47561	Interferon-recepto
2	42	100.0	18	15	AAR47562	Interferon-recepto
3	42	100.0	90	21	AAY55987	Partial human inte
4	42	100.0	133	3	AAP20109	Sequence encoded b
5	42	100.0	150	12	AAR11799	Interferon alpha 8
6	42	100.0	162	6	AAP50168	Sequence of hybrid
7	42	100.0	165	4	AAP30687	Thr14, Met16 mutan
8	42	100.0	165	18	AAW43382	Human interferon-a
9	42	100.0	165	18	AAW43386	Human interferon-a
10	42	100.0	165	18	AAW43387	Human interferon-a
11	42	100.0	165	18	AAW43390	Human interferon-a
12	42	100.0	165	20	AAY43492	A human interferon
13	42	100.0	165	21	AAY82887	N-terminal modifie
14	42	100.0	165	21	AAY44828	Hybrid interferon
15	42	100.0	165	21	AAY44976	Human hybrid inter
16	42	100.0	166	4	AAP30683	Synthetic human le
17	42	100.0	166	4	AAP30684	Consensus human le
18	42	100.0	166	4	AAP30685	Consensus human le
19	42	100.0	166	4	AAP30686	Consensus human le
20	42	100.0	166	6	AAP50229	Interferon alpha-1
21	42	100.0	166	7	AAP60828	Sequence of interf
22	42	100.0	166	7	AAP60100	Sequence of hybrid
23	42	100.0	166	7	AAP60102	Sequence of hybrid
24	42	100.0	166	7	AAP60103	Sequence of hybrid
25	42	100.0	166	7	AAP60304	Sequence of interf
26	42	100.0	166	10	AAP90186	Hybrid alpha-inter
27	42	100.0	166	10	AAP90188	Hybrid alpha-inter
28	42	100.0	166	10	AAP90189	Hybrid alpha-inter
29	42	100.0	166	14	AAR42813	Lymphoblastoid int
30	42	100.0	166	16	AAR67761	Interferon-alpha-6
31	42	100.0	166	16	AAR67762	Interferon-alpha-7
32	42	100.0	166	18	AAW43380	Human interferon-a
33	42	100.0	166	20	AAY43491	A human interferon
34	42	100.0	166	20	AAY05813	Human interferon-a
35	42	100.0	166	20	AAY05806	Human interferon-a
36	42	100.0	166	20	AAY05807	Human interferon-a
37	42	100.0	166	20	AAY05808	Human interferon-a
38	42	100.0	166	20	AAY05809	Human interferon-a
39	42	100.0	166	20	AAY05810	Human interferon-a
40	42	100.0	166	20	AAY05811	Human interferon-a
41	42	100.0	166	20	AAY05812	Human interferon-a
42	42	100.0	166	21	AAB07339	Mature human IFNal
43	42	100.0	166	21	AAB07341	Mutant human IFNal
44	42	100.0	166	21	AAB07345	Mutant human IFNal
45	42	100.0	166	21	AAB07346	Mutant human IFNal

ALIGNMENTS

RESULT 1
AAR47561
ID AAR47561 standard; peptide; 11 AA.
XX
AC AAR47561;
XX
DT 12-JUL-1994 (first entry)
XX
DE Interferon-receptor binding peptide #4.
XX
KW IFN; cell surface receptor; pharmaceutical carrier molecule;
KW drug delivery; neoplastic tissue; infection;
KW Type 1 human interferon receptor complex.
XX
OS Synthetic.
XX
PN WO9401457-A.
XX
PD 20-JAN-1994.
XX
PF 06-JUL-1993; 93WO-CA00279.
XX
PR 07-JUL-1992; 92US-0909739.
PR 20-NOV-1992; 92US-0980525.
XX
PA (FISH/) FISH E N.
XX
PI Fish EN;
XX
DR WPI; 1994-034987/04.
XX
PT New interferon receptor-binding peptide(s) - useful for
PT delivering a pharmaceutically active drug to cells, e.g.
PT neoplastic, infected or inflamed tissue cells

```
XX
PS   Claim 4; Page 35; 51pp; English.
XX
CC   The critical clusters of amino acids in the different IFN-alphas and
CC   IFN-beta that interact with the Type 1 IFN receptor complex were
CC   defined. These critical peptide domains were used to design
CC   synthetic peptides AAR47558-R47564 that are useful as carriers for
CC   pharmaceutical compositions.
XX
SQ   Sequence   11 AA;


  Query Match           100.0%;  Score 42;  DB 15;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 0.075;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db      2 ltekkysp 9


RESULT   2
AAR47562
ID   AAR47562 standard; peptide; 18 AA.
XX
AC   AAR47562;
XX
DT   12-JUL-1994  (first entry)
XX
DE   Interferon-receptor binding peptide #5.
XX
KW   IFN; cell surface receptor; pharmaceutical carrier molecule;
KW   drug delivery; neoplastic tissue; infection;
KW   Type 1 human interferon receptor complex.
XX
OS   Synthetic.
XX
PN   WO9401457-A.
XX
PD   20-JAN-1994.
XX
PF   06-JUL-1993;   93WO-CA00279.
XX
PR   07-JUL-1992;   92US-0909739.
PR   20-NOV-1992;   92US-0980525.
XX
PA   (FISH/) FISH E N.
XX
PI   Fish EN;
XX
DR   WPI; 1994-034987/04.
XX
PT   New interferon receptor-binding peptide(s) - useful for
PT   delivering a pharmaceutically active drug to cells, e.g.
PT   neoplastic, infected or inflamed tissue cells
XX
PS   Claim 5; Page 35; 51pp; English.
XX
CC   The critical clusters of amino acids in the different IFN-alphas and
CC   IFN-beta that interact with the Type 1 IFN receptor complex were
CC   defined. These critical peptide domains were used to design
CC   synthetic peptides AAR47558-R47564 that are useful as carriers for
CC   pharmaceutical compositions.
XX
SQ   Sequence   18 AA;


  Query Match           100.0%;  Score 42;  DB 15;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 0.13;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db      9 ltekkysp 16


RESULT   3
AAY55987
ID   AAY55987 standard; Protein; 90 AA.
XX
AC   AAY55987;
XX
DT   15-MAR-2000  (first entry)
XX
DE   Partial human interferon-alpha5 protein.
XX
KW   Antiviral; anticancer; antiproliferative; human; interferon-alpha5;
KW   hepatic disease; hepatitis C; viral cirrhosis; hepatocellular carcinoma;
KW   liver; gene expression.
XX
OS   Homo sapiens.
XX
PN   WO9958143-A1.
XX
PD   18-NOV-1999.
XX
PF   13-MAY-1999;   99WO-ES00134.
XX
PR   13-MAY-1998;   98ES-0001003.
XX
PA   (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.
XX
PI   Prieto Valtuena J,  Civeira Murillo MP,  Larrea Leoz E;
XX
DR   WPI; 2000-038959/03.
DR   N-PSDB; AAZ47031.
XX
PT   Treating liver diseases with interferon-alpha5 or nucleic acid encoding
PT   it, particularly chronic hepatitis C  -
XX
PS   Disclosure; Page 30; 36pp; Spanish.
XX
CC   This sequence corresponds to a fragment of the human interferon-alpha5
CC   protein (GenBank Accession No: X02956).  The invention relates to a
CC   method of using interferon-alpha5 or its coding sequence to prepare
CC   compositions for treatment of hepatic diseases, e.g. (i) chronic
CC   hepatitis C; (ii) cirrhosis of viral origin and (iii) hepatocellular
CC   carcinoma. The method restores the level of interferon-alpha5, which
CC   is reduced in diseased liver cells, to normal levels.
XX
SQ   Sequence   90 AA;


  Query Match           100.0%;  Score 42;  DB 21;  Length 90;
  Best Local Similarity  100.0%;  Pred. No. 0.68;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db     74 ltekkysp 81


RESULT   4
AAP20109
ID   AAP20109 standard; Protein; 133 AA.
XX
AC   AAP20109;
XX
DT   10-AUG-1992  (first entry)
XX
DE   Sequence encoded by leukocyte interferon LeIF G cDNA.
XX
KW   Viral infection; therapy; malignancy.
XX
OS   Homo sapiens.
XX
```

PN GB2079291-A.
XX
PD 20-JAN-1982.
XX
PF 01-JUL-1981; 81GB-0120279.
XX
PR 21-APR-1981; 81US-0256204.
PR 01-JUL-1980; 80US-0164986.
PR 08-SEP-1980; 80US-0184909.
PR 10-NOV-1980; 80US-0205578.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
PA (GENE-) GENENTECH INC.
XX
PI Goeddel DVN, Pestka S;
XX
DR WPI; 1982-04460E/03.
DR N-PSDB; AAN20096.
XX
PT Mature human leukocyte interferon polypeptide(s) - prepd. from
PT microbes transformed with appropriate DNA sequences
XX
PS Example; Fig 4; 20pp; English.
XX
CC The inventors claim a polypeptide comprising the AA sequence of a
CC mature human LeIF and a DNA sequence encoding it. LeIF A-D, F, H-J
CC and encoding DNA are specifically claimed. They are natural allelic
CC variations. LeIF is isolated from the leukocytes of humans with
CC chronic myelogenous leukaemia, induced to produce interferon with
CC Sendai or Newcastle disease virus; esp. the cell line KG-1.
XX
SQ Sequence 133 AA;

Query Match 100.0%; Score 42; DB 3; Length 133;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 98 ltekkysp 105

RESULT 5
AAR11799
ID AAR11799 standard; Protein; 150 AA.
XX
AC AAR11799;
XX
DT 03-JUN-1991 (first entry)
XX
DE Interferon alpha 88 as CR2 ligand.
XX
KW Cellular receptor 2; CR2; binding site; BS; auto-immune disease;
KW Epstein-Barr Virus; EBV; B lymphocyte; ligand; interferon alpha 88.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Binding-site 72..86
FT /note= "fragment pref. included"
FT Binding-site 75..82
FT /note= "fragment most pref. included"
XX
PN WO9103251-A.
XX
PD 21-MAR-1991.
XX
PF 04-SEP-1990; 90WO-US05027.
XX
PR 20-APR-1990; 90US-0512118.
PR 08-SEP-1989; 89US-0404679.
XX
PA (CALB-) CALIF INST BIOLOGIC.
XX
PI Lernhardt W;
XX
DR WPI; 1991-101864/14.
XX
PT DNA segment encoding CR-2 ligand and CR2 binding site - used to
PT treat auto-immune disease, B-cell lymphoma and inhibit
PT Epstein-Barr virus infection
XX
PS Disclosure; Fig 2; 129pp; English.
XX
CC The ligand pref. includes the fragment indicated in the features.
CC The ligand pref. contains only a single BS and has an amino acid
CC sequence <100 (pref. <20) residues in length.
CC The ligand may also comprise a plurality of fragment 75..82.
CC A therapeutic compsn. contg. the polypeptide is used to stimulate
CC or inhibit B lymphocyte proliferation in patients with B cell
CC lymphoma. B lymphocytes and myeloma's can be stimulated in
CC patients with immunodeficiencies and immunoglobulin secretion by
CC hybridoma cultures can be boosted.
CC The compsn. can be administered to inhibit infection in vitro or in
CC vivo by Epstein-Barr Virus.
CC See also AAQ11140-42 and AAR11355 for IFN alpha.
XX
SQ Sequence 150 AA;

Query Match 100.0%; Score 42; DB 12; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 115 ltekkysp 122

RESULT 6
AAP50168
ID AAP50168 standard; Protein; 162 AA.
XX
AC AAP50168;
XX
DT 30-OCT-1991 (first entry)
XX
DE Sequence of hybrid alpha interferon (alpha-IFN).
XX
KW Antiviral agent; antitumour; interferon-alpha; virucide;
KW immunostimulant.
XX
OS Homo sapiens.
XX
PN EP146903-A.
XX
PD 03-JUL-1985.
XX
PF 17-DEC-1984; 84EP-0115623.
XX
PR 21-DEC-1983; 83US-0564066.
PR 19-DEC-1983; 83US-0562639.
XX
PA (SCHE) SCHERING CORP.
XX
PI Leibowitz PJ, Ryan MJ;
XX
DR WPI; 1985-160612/27.
DR N-PSDB; AAN50236.
XX
PT New hybrid alpha-interferon with enhanced antiviral activity -
PT prepd. by recombinant DNA procedures
XX
PS Claim 2; Page 22; 26pp; English.
XX

```
CC   The hybrid alpha-IFN of the invention includes different portions of
CC   two different naturally occurring alpha-IFN as joined discrete sub-
CC   sequences. They are defined and arranged as a delta-4 alpha-2
CC   (Bgl II-1) sub-segment preceding a (Bgl II) alpha-1 segment. It has
CC   an antiviral activity of at least 100,000,000 units/mg by cytopathic
CC   effect-inhibition assay. Dose is 100,000 - 1000,000,000 units/square
CC   metre body surface daily topically. The N-terminal Met is optional.
CC   The claimed DNA sequence coding for the hybrid alpha-IFN may differ
CC   in accordance with the degeneracy of the genetic code.
XX
SQ   Sequence   162 AA;

  Query Match            100.0%;  Score 42;  DB 6;  Length 162;
  Best Local Similarity  100.0%;  Pred. No. 1.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    127 ltekkysp 134


RESULT   7
AAP30687
ID   AAP30687 standard; Protein; 165 AA.
XX
AC   AAP30687;
XX
DT   10-SEP-1992  (first entry)
XX
DE   Thr14, Met16 mutant human leukocyte interferon subtype F.
XX
KW   Mutation; human; IFN.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          14
FT                   /note= "mutation, Ala -> Thr"
FT   Region          16
FT                   /note= "mutation, Ile -> Met"
XX
PN   WO8304053-A.
XX
PD   24-NOV-1983.
XX
PF   25-APR-1983;   83WO-US00605.
XX
PR   15-APR-1983;   83US-0483451.
PR   06-MAY-1982;   82US-0375494.
PR   12-DEC-1983;   83US-0560495.
PR   21-SEP-1987;   87US-0099096.
PR   01-JAN-1990;   90EP-0124236.
XX
PA   (AMGE-) AMGEN INC.
PA   (AMGE-) AMGEN.
PA   (MOLE-) APPL MOLECULAR GENE.
XX
PI   Alton NK,  Peters MA,  Stabinsky Y,  Snitman DL;
XX
DR   WPI; 1983-833208/48.
XX
PT   Construction of large structural genes - useful in prepn. of
PT   human leukocyte interferon and analogues
XX
PS   Claim 46; Page 85; 94pp; English.
XX
CC   The sequence is that of a polypeptide which differs from human
CC   leukocyte interferon subtype F by two amino acid substitutions.
CC   It may be recombinantly produced in micro organisms transformed
CC   with the manufactured gene encoding it. See also AAP30673-P30686.
XX
SQ   Sequence   165 AA;

  Query Match            100.0%;  Score 42;  DB 4;  Length 165;
  Best Local Similarity  100.0%;  Pred. No. 1.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    131 ltekkysp 138


RESULT   8
AAW43382
ID   AAW43382 standard; protein; 165 AA.
XX
AC   AAW43382;
XX
DT   07-APR-1998  (first entry)
XX
DE   Human interferon-alpha 2b mutant (K132T).
XX
KW   Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;
KW   nucleic acid binding agent; targeted expression; mutant.
XX
OS   Homo sapiens.
XX
PN   WO9733998-A1.
XX
PD   18-SEP-1997.
XX
PF   14-MAR-1997;   97WO-US03846.
XX
PR   14-MAR-1996;   96US-0616023.
XX
PA   (IMMU-) IMMUNE RESPONSE CORP.
XX
PI   Carlo DJ,  Chiou HC;
XX
DR   WPI; 1997-470878/43.
XX
PT   Delivering interferon gene to target mammalian cells in vivo or in
PT   vitro - as a molecular complex with a conjugate of nucleic acid
PT   binding agent and ligand for cell surface receptor, e.g. for
PT   treating virus infection or tumours
XX
PS   Disclosure; Figure 11B; 52pp; English.
XX
CC   This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)
CC   mutant (K132T) which was recombinantly expressed in mice. A series
CC   of IFN-alpha 2b mutants were prepared with various single amino acid
CC   substitutions (AAW43382-90). The effect of these substitutions on
CC   antiviral activity (on mouse cells) for human IFN-alpha 2b was
CC   compared. This mutant had a relative activity of 0.1 compared with
CC   the native IFN-alpha 2b. The invention relates to a complex which
CC   targets expression of interferon in selected cells. The complex
CC   comprises the gene encoding interferon releasably linked to a conjugate
CC   of nucleic acid binding agent and a ligand which binds to a component on
CC   the surface of the cell. The method is used for targeted expression of
CC   recombinant IFN in selected cells, in vivo or in vitro, particularly for
CC   treatment of hepatitis, several forms of cancer and leukaemia and
CC   condyloma acuminatum, or for production of IFN for subsequent
CC   administration as exogenous protein.
XX
SQ   Sequence   165 AA;

  Query Match            100.0%;  Score 42;  DB 18;  Length 165;
  Best Local Similarity  100.0%;  Pred. No. 1.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    130 ltekkysp 137
```

```
RESULT   9
AAW43386
ID   AAW43386 standard; protein; 165 AA.
XX
AC   AAW43386;
XX
DT   07-APR-1998  (first entry)
XX
DE   Human interferon-alpha 2b mutant (Q125R; K132T).
XX
KW   Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;
KW   nucleic acid binding agent; targeted expression; mutant.
XX
OS   Homo sapiens.
XX
PN   WO9733998-A1.
XX
PD   18-SEP-1997.
XX
PF   14-MAR-1997;   97WO-US03846.
XX
PR   14-MAR-1996;   96US-0616023.
XX
PA   (IMMU-) IMMUNE RESPONSE CORP.
XX
PI   Carlo DJ,  Chiou HC;
XX
DR   WPI; 1997-470878/43.
XX
PT   Delivering interferon gene to target mammalian cells in vivo or in
PT   vitro - as a molecular complex with a conjugate of nucleic acid
PT   binding agent and ligand for cell surface receptor, e.g. for
PT   treating virus infection or tumours
XX
PS   Disclosure; Figure 11B; 52pp; English.
XX
CC   This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)
CC   mutant (Q125R; K132T) which was recombinantly expressed in mice. A
CC   series of IFN-alpha 2b mutants were prepared with various amino acid
CC   substitutions (AAW43382-90). The effect of these substitutions on
CC   antiviral activity (on mouse cells) for human IFN-alpha 2b was
CC   compared. This mutant had a relative activity of 23 compared with
CC   the native IFN-alpha 2b. The invention relates to a complex which
CC   targets expression of interferon in selected cells. The complex
CC   comprises the gene encoding interferon releasably linked to a conjugate
CC   of nucleic acid binding agent and a ligand which binds to a component on
CC   the surface of the cell. The method is used for targeted expression of
CC   recombinant IFN in selected cells, in vivo or in vitro, particularly for
CC   treatment of hepatitis, several forms of cancer and leukaemia and
CC   condyloma acuminatum, or for production of IFN for subsequent
CC   administration as exogenous protein.
XX
SQ   Sequence   165 AA;


  Query Match             100.0%;  Score 42;  DB 18;  Length 165;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db     130 ltekkysp 137


RESULT  10
AAW43387
ID   AAW43387 standard; protein; 165 AA.
XX
AC   AAW43387;
XX
DT   07-APR-1998  (first entry)
XX
DE   Human interferon-alpha 2b mutant (R121K; Q125R; K132T).
XX
KW   Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;
KW   nucleic acid binding agent; targeted expression; mutant.
XX
OS   Homo sapiens.
XX
PN   WO9733998-A1.
XX
PD   18-SEP-1997.
XX
PF   14-MAR-1997;   97WO-US03846.
XX
PR   14-MAR-1996;   96US-0616023.
XX
PA   (IMMU-) IMMUNE RESPONSE CORP.
XX
PI   Carlo DJ,  Chiou HC;
XX
DR   WPI; 1997-470878/43.
XX
PT   Delivering interferon gene to target mammalian cells in vivo or in
PT   vitro - as a molecular complex with a conjugate of nucleic acid
PT   binding agent and ligand for cell surface receptor, e.g. for
PT   treating virus infection or tumours
XX
PS   Disclosure; Figure 11B; 52pp; English.
XX
CC   This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)
CC   mutant (R121K; Q125R; K132T) which was recombinantly expressed in mice.
CC   A series of IFN-alpha 2b mutants were prepared with various amino acid
CC   substitutions (AAW43382-90). The effect of these substitutions on
CC   antiviral activity (on mouse cells) for human IFN-alpha 2b was
CC   compared. This mutant had a relative activity of 170 compared with
CC   the native IFN-alpha 2b. The invention relates to a complex which
CC   targets expression of interferon in selected cells. The complex
CC   comprises the gene encoding interferon releasably linked to a conjugate
CC   of nucleic acid binding agent and a ligand which binds to a component on
CC   the surface of the cell. The method is used for targeted expression of
CC   recombinant IFN in selected cells, in vivo or in vitro, particularly for
CC   treatment of hepatitis, several forms of cancer and leukaemia and
CC   condyloma acuminatum, or for production of IFN for subsequent
CC   administration as exogenous protein.
XX
SQ   Sequence   165 AA;


  Query Match             100.0%;  Score 42;  DB 18;  Length 165;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db     130 ltekkysp 137


RESULT  11
AAW43390
ID   AAW43390 standard; protein; 165 AA.
XX
AC   AAW43390;
XX
DT   07-APR-1998  (first entry)
XX
DE   Human interferon-alpha 2b mutant (Q125K; K132T).
XX
KW   Gene delivery; interferon-alpha 2b; IFN-alpha 2b; IFN-beta; IFN-gamma;
KW   nucleic acid binding agent; targeted expression; mutant.
XX
OS   Homo sapiens.
XX
PN   WO9733998-A1.
```

XX
PD 18-SEP-1997.
XX
PF 14-MAR-1997; 97WO-US03846.
XX
PR 14-MAR-1996; 96US-0616023.
XX
PA (IMMU-) IMMUNE RESPONSE CORP.
XX
PI Carlo DJ, Chiou HC;
XX
DR WPI; 1997-470878/43.
XX
PT Delivering interferon gene to target mammalian cells in vivo or in
PT vitro - as a molecular complex with a conjugate of nucleic acid
PT binding agent and ligand for cell surface receptor, e.g. for
PT treating virus infection or tumours
XX
PS Disclosure; Figure 11B; 52pp; English.
XX
CC This sequence represents a human interferon-alpha 2b (IFN-alpha 2b)
CC mutant (Q125K; K132T) which was recombinantly expressed in mice. A
CC series of IFN-alpha 2b mutants were prepared with various amino acid
CC substitutions (AAW43382-90). The effect of these substitutions on
CC antiviral activity (on mouse cells) for human IFN-alpha 2b was
CC compared. This mutant had a relative activity of 45 compared with
CC the native IFN-alpha 2b. The invention relates to a complex which
CC targets expression of interferon in selected cells. The complex
CC comprises the gene encoding interferon releasably linked to a conjugate
CC of nucleic acid binding agent and a ligand which binds to a component on
CC the surface of the cell. The method is used for targeted expression of
CC recombinant IFN in selected cells, in vivo or in vitro, particularly for
CC treatment of hepatitis, several forms of cancer and leukaemia and
CC condyloma acuminatum, or for production of IFN for subsequent
CC administration as exogenous protein.
XX
SQ Sequence 165 AA;

Query Match 100.0%; Score 42; DB 18; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 130 ltekkysp 137

RESULT 12
AAY43492
ID AAY43492 standard; Protein; 165 AA.
XX
AC AAY43492;
XX
DT 26-JAN-2000 (first entry)
XX
DE A human interferon-alpha (IFN-alpha) protein.
XX
KW Interferon-alpha-2b; IFN-alpha; avb3 antagonist; avb3 receptor ligand;
KW metastasis-associated receptor ligand; angiogenesis; cell proliferation;
KW anti-angiogenic protein; avb3-integrin; cancer; arthritis;
KW macular degeneration; diabetic retinopathy; hemangioma; psoriasis;
KW osteoporosis; thrombosis; angina; atherosclerosis; antiviral;
KW antibacterial; antifungal.
XX
OS Homo sapiens.
XX
PN WO9951638-A1.
XX
PD 14-OCT-1999.
XX
PF 07-APR-1999; 99WO-US04295.
XX
PR 08-APR-1998; 98US-0081074.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Tjoeng FS, Fok KF;
XX
DR WPI; 1999-620196/53.
XX
PT New conjugates of integrin antagonist and ligand for
PT metastasis-associated receptor, for treating angiogenesis-related
PT diseases, e.g. cancer -
XX
PS Claim 12; Page 102; 108pp; English.
XX
CC The present sequence represents an interferon-alpha (IFN-alpha) protein,
CC and can be conjugated to the avb3 antagonists of the invention. The
CC specification describes pharmaceutical compounds and their salts which
CC are dual avb3 receptor/metastasis-associated receptor ligands. These
CC compounds inhibit angiogenesis and thus proliferation of (cancer) cells.
CC One component binds to the avb3 receptor and the other to a
CC metastasis-associated receptor. The avb3 antagonists may also be
CC conjugated to anti-angiogenic proteins, such as IFN-alpha and its
CC derivatives. The compounds are used to treat angiogenesis-related
CC disorders (mediated by the avb3-integrin), specifically cancer (of lung,
CC breast, ovary, prostate, stomach, colon, kidney or bladder, also
CC melanoma, hepatoma, sarcoma and lymphoma), arthritis and macular
CC degeneration, and also diabetic retinopathy, hemangioma, psoriasis,
CC osteoporosis, thrombosis, angina, atherosclerosis etc. The compounds may
CC also be useful as antiviral, antibacterial and antifungal agents.
XX
SQ Sequence 165 AA;

Query Match 100.0%; Score 42; DB 20; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 130 ltekkysp 137

RESULT 13
AAY82887
ID AAY82887 standard; Protein; 165 AA.
XX
AC AAY82887;
XX
DT 25-JUL-2000 (first entry)
XX
DE N-terminal modified interferon alpha A/D hybrid.
XX
KW Biconjugate; a_vb_3 integrin; interferon alpha; angiogenesis;
KW cancer; tumour; osteoporosis; Paget's disease; Karposi's sarcoma;
KW periodontal disease; metastasis; neoplasia; retinopathy; arthritis;
KW psoriasis; leukaemia; malignant melanoma; atherosclerosis;
KW smooth muscle cell migration; inhibition; treatment; antagonist;
KW angina; thrombosis; restenosis; antiviral; antifungal;
KW antibacterial.
XX
OS Homo sapiens.
XX
PN WO200009143-A1.
XX
PD 24-FEB-2000.
XX
PF 07-APR-1999; 99WO-US04296.
XX
PR 13-AUG-1998; 98US-0096442.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Fok KF, Tjoeng FS;

```
XX
DR   WPI; 2000-205894/18.
DR   N-PSDB; AAZ93036.
XX
PT   New bioconjugates comprising an avb3 antagonist and a
PT   metastatic-associated receptor ligand, useful for treating cancer and
PT   other angiogenic diseases, or as antiviral, antifungal or antibacterial
PT   agents -
XX
PS   Claim 13; Page 111; 123pp; English.
XX
CC   Bioconjugates comprising one or more a_vb_3 antagonist moieties
CC   coupled to a peptide or polypeptide having anti-angiogenic properties
CC   can be used for treating a human patient with an
CC   angiogenesis-mediated disease, e.g. cancer, arthritis, or macular
CC   degeneration. The a_vb_3 integrin is normally associated with
CC   endothelial cells but can promote the formation of blood vessels
CC   (angiogenesis) in tumours. The a_vb_3 integrin is also known to
CC   play a role in tumour metastasis, neoplasia, osteoporosis,
CC   Paget's disease, retinopathy, arthritis, periodontal disease,
CC   psoriasis and smooth muscle cell migration. Interferon alpha is a
CC   family of proteins which possess complex antiviral, antineoplastic
CC   and immunomodulating activities. Interferon alpha is effective
CC   against a variety of cancers including hairy cell leukaemia,
CC   chronic myelogenous leukaemia, malignant melanoma and Karposi's
CC   sarcoma. Multi-functional bioconjugates comprising both a_vb_3
CC   antagonists and interferon alpha 2b can exhibit greater biological
CC   activity when compared to a single factor or having improved
CC   half-life or decreased adverse side effects, or a combination of
CC   these properties. They can be used for inhibiting elevated levels
CC   of tumor antigens, inhibiting the proliferation of tumor cells and
CC   inhibiting tumor growth. The bioconjugates can also be used for
CC   treating e.g. osteoporosis, humoral hypercalcemia of malignancy,
CC   Paget's disease, retinopathy including diabetic retinopathy,
CC   arthritis, including rheumatoid arthritis, periodontal disease,
CC   psoriasis, thrombosis, angina, atherosclerosis, smooth muscle cell
CC   migration and restenosis in a mammal. They are also useful as
CC   antiviral, antifungal and antibacterial agents. pMON20433 is a
CC   modified version of pMON20405 (See AAZ93035) such that the amino
CC   terminus of interferon alpha A/D is Met-Cys-IFN alpha A/D as
CC   opposed to Met-Ala-Cys-IFN alpha A/D.
XX
SQ   Sequence   165 AA;


  Query Match             100.0%;  Score 42;  DB 21;  Length 165;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db     130 ltekkysp 137


RESULT  14
AAY44828
ID   AAY44828 standard; Protein; 165 AA.
XX
AC   AAY44828;
XX
DT   18-MAY-2000  (first entry)
XX
DE   Hybrid interferon fusion protein HY-3.
XX
KW   Hybrid interferon-alpha protein; HY-3; IFN-alpha; antiviral;
KW   antiproliferative; influenza; hepatitis B; cell growth regulation;
KW   tumour; cancer; osteogenic sarcoma; multiple myeloma.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200006735-A1.
XX
PD   10-FEB-2000.
XX
PF   06-JUL-1999;   99WO-US15284.
XX
PR   28-JUL-1998;   98US-0094407.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Zoon KC,  Hu R,  Bekisz JB,  Hayes MP;
XX
DR   WPI; 2000-183128/16.
DR   N-PSDB; AAZ50311.
XX
PT   New hybrid interferon-alpha polypeptides with interferon-alpha
PT   biological activity, useful to treat viral diseases -
XX
PS   Claim 8; Fig 5; 72pp; English.
XX
CC   The present sequence is hybrid interferon fusion protein HY-3,
CC   comprising IFN-alpha 2c (amino acid residues 96-166) and IFN-alpha21a
CC   (amino acid residues 1-95). This is used as an antiviral and
CC   antiproliferative agent. Hybrid IFN-alpha (interferon-alpha) proteins
CC   are used in the treatment of viral diseases e.g. influenza, hepatitis B,
CC   or to regulate cell growth, especially tumour cell growth e.g. in tumour
CC   treatment and cancers like osteogenic sarcoma, multiple myeloma etc.
CC   They are transformed into host cells using vectors. Pharmaceutically
CC   acceptable carriers can be included with hybrid IFN-alpha for
CC   therapeutic administration.
XX
SQ   Sequence   165 AA;


  Query Match             100.0%;  Score 42;  DB 21;  Length 165;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db     130 ltekkysp 137


RESULT  15
AAY44976
ID   AAY44976 standard; Protein; 165 AA.
XX
AC   AAY44976;
XX
DT   23-MAY-2000  (first entry)
XX
DE   Human hybrid interferon alpha, HY-3.
XX
KW   Human; Interferon alpha; HuIFNalpha; hybrid; HY-3; IFN-alpha21a; tumour;
KW   IFN-alpha2c; cytostatic; antiviral; antiproliferative; immunomodulator;
KW   treatment; viral disease; encephalomyocarditis; influenza; rabies;
KW   respiratory tract infection; viral zoonoses; arbovirus infection;
KW   Herpes simplex; Varicella zoster; keratitis; Hodgkin's disease; cancer;
KW   acute haemorrhagic conjunctivitis; hepatitis B; hepatitis C; lymphoma;
KW   osteogenic sarcoma; multiple myeloma; leukaemia; carcinoma; melanoma;
KW   papilloma.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1..95
FT                   /note= "Derived from IFN-alpha2c"
FT   Domain          76..166
FT                   /note= "Domain affecting antiproliferative activity"
FT   Region          96..166
FT                   /note= "Derived from IFN-alpha21a"
XX
PN   WO200006596-A2.
XX
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PD 10-FEB-2000.
XX
PF 29-JUN-1999; 99WO-US14749.
XX
PR 28-JUL-1998; 98US-0094407.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Zoon KC, Hu R, Bekisz JB, Hayes MP;
XX
DR WPI; 2000-195259/17.
DR N-PSDB; AAZ50512.
XX
PT Novel human hybrid interferons and their mutants, useful for treating
PT viral infections such as rabies and hepatitis B and C, and cancers such
PT as melanoma, multiple myeloma, and papilloma -
XX
PS Claim 10; Page 49-50; 66pp; English.
XX
CC The present amino acid sequence is the human hybrid interferon-alpha
CC (HuIFNalpha) polypeptide HY-3, comprising a fusion of IFN-alpha2la and
CC IFN-alpha2c. This hybrid IFN has antiviral, antiproliferative,
CC cytostatic and immunomodulator activity. HY-3 exhibited a higher
CC antiproliferative activity than the parental interferons, IFN-alpha2c
CC and IFN-alpha2la and other IFN-alpha hybrids.
CC Hybrid IFNs are used for treatment of viral diseases, such as
CC encephalomyocarditis, influenza, respiratory tract infections, rabies,
CC viral zoonoses, arbovirus, Herpes simplex and Varicella zoster
CC infections, keratitis, acute haemorrhagic conjunctivitis and hepatitis B
CC and C. It is also used for modulation of immune system, regulation of
CC tumour growth and cancers such as osteogenic sarcoma, multiple myeloma,
CC Hodgkin's disease, nodular, poorly differentiated lymphoma, acute
CC lymphocytic leukaemia, acute myeloid leukaemia, breast carcinoma,
CC melanoma, papilloma and nasopharyngeal carcinoma in humans.
XX
SQ Sequence 165 AA;

Query Match 100.0%; Score 42; DB 21; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 130 ltekkysp 137

Search completed: December 13, 2001, 10:46:23
Job time: 103 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:44:40 ; Search time 181.51 Seconds
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Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	42	100.0	8	18	US-09-424-080-1	Sequence 1, Appli
2	42	100.0	11	3	US-07-980-525-4	Sequence 4, Appli
3	42	100.0	11	13	US-08-920-579-4	Sequence 4, Appli
4	42	100.0	18	3	US-07-980-525-5	Sequence 5, Appli
5	42	100.0	18	13	US-08-920-579-5	Sequence 5, Appli
6	42	100.0	30	11	US-08-769-062-79	Sequence 79, Appl
7	42	100.0	46	24	US-60-182-467-1317	Sequence 1317, Ap
8	42	100.0	60	24	US-60-163-123-1406	Sequence 1406, Ap
9	42	100.0	70	24	US-60-177-571-2851	Sequence 2851, Ap
10	42	100.0	71	24	US-60-177-571-2858	Sequence 2858, Ap
11	42	100.0	72	16	US-09-275-278-11	Sequence 11, Appl
12	42	100.0	73	24	US-60-177-571-2852	Sequence 2852, Ap
13	42	100.0	73	24	US-60-177-571-2853	Sequence 2853, Ap
14	42	100.0	73	24	US-60-177-571-2854	Sequence 2854, Ap
15	42	100.0	73	24	US-60-177-571-2855	Sequence 2855, Ap
16	42	100.0	73	24	US-60-177-571-2856	Sequence 2856, Ap
17	42	100.0	73	24	US-60-177-571-2857	Sequence 2857, Ap
18	42	100.0	73	24	US-60-177-571-2859	Sequence 2859, Ap
19	42	100.0	73	24	US-60-177-571-2860	Sequence 2860, Ap
20	42	100.0	73	24	US-60-177-571-2861	Sequence 2861, Ap
21	42	100.0	73	24	US-60-177-571-2862	Sequence 2862, Ap
22	42	100.0	77	24	US-60-163-123-1760	Sequence 1760, Ap
23	42	100.0	111	24	US-60-196-718-5609	Sequence 5609, Ap
24	42	100.0	133	2	US-06-256-204-14	Sequence 14, Appl
25	42	100.0	133	2	US-06-256-204-23	Sequence 23, Appl
26	42	100.0	133	24	US-60-163-123-1012	Sequence 1012, Ap
27	42	100.0	133	24	US-60-163-123-1197	Sequence 1197, Ap
28	42	100.0	150	3	US-07-980-525-10	Sequence 10, Appl
29	42	100.0	150	3	US-07-980-525-11	Sequence 11, Appl
30	42	100.0	150	3	US-07-980-525-12	Sequence 12, Appl
31	42	100.0	150	13	US-08-920-579-10	Sequence 10, Appl
32	42	100.0	150	13	US-08-920-579-11	Sequence 11, Appl
33	42	100.0	150	13	US-08-920-579-12	Sequence 12, Appl
34	42	100.0	162	3	US-07-980-525-15	Sequence 15, Appl
35	42	100.0	162	13	US-08-920-579-15	Sequence 15, Appl
36	42	100.0	162	24	US-60-196-718-5608	Sequence 5608, Ap
37	42	100.0	163	24	US-60-196-718-5607	Sequence 5607, Ap
38	42	100.0	163	24	US-60-196-718-5610	Sequence 5610, Ap
39	42	100.0	163	24	US-60-196-718-5611	Sequence 5611, Ap
40	42	100.0	163	24	US-60-196-718-5613	Sequence 5613, Ap
41	42	100.0	165	3	US-07-980-525-13	Sequence 13, Appl
42	42	100.0	165	3	US-07-980-525-14	Sequence 14, Appl
43	42	100.0	165	13	US-08-920-579-13	Sequence 13, Appl
44	42	100.0	165	13	US-08-920-579-14	Sequence 14, Appl
45	42	100.0	165	16	US-09-283-390-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-424-080-1
; Sequence 1, Application US/09424080
; GENERAL INFORMATION:
; APPLICANT: ZAVIALOV, Vladimir et al.
; TITLE OF INVENTION: COMPOSITION FOR ENHANCING IMMUNOSUPPERSANTS PHARMACEUTICAL ACT
; FILE REFERENCE: 0933-0149P
; CURRENT APPLICATION NUMBER: US/09/424,080
; CURRENT FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunosupressants cylcoporins, FK506, or rapamycin sequences
; OTHER INFORMATION: derived from various organisms using sequence alignment.
US-09-424-080-1

Query Match 100.0%; Score 42; DB 18; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 1 LTEKKYSP 8

RESULT 2
US-07-980-525-4

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; Sequence 4, Application US/07980525
; GENERAL INFORMATION:
;   APPLICANT:  FISH, Eleanor N.
;   TITLE OF INVENTION:  INTERFERON RECEPTOR BINDING PEPTIDES
;   NUMBER OF SEQUENCES:  17
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram
;     STREET:  655 Fifteenth Street N.W. Suite 330
;     CITY:  Washington
;     STATE:  D.C.
;     COUNTRY:  U.S.A.
;     ZIP:  20005-5701
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/07/980,525
;     FILING DATE:  19921120
;     CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US/07/909,738
;     FILING DATE:  07-JUL-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Murray, Robert B.
;     REGISTRATION NUMBER:  22,980
;     REFERENCE/DOCKET NUMBER:  638-2005
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (202)638-5000
;     TELEFAX:  (202)638-4810
; INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  11 amino acids
;     TYPE:  AMINO ACID
;     TOPOLOGY:  unknown
;   MOLECULE TYPE:  peptide
US-07-980-525-4


  Query Match             100.0%;  Score 42;  DB 3;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
Db       2 LTEKKYSP 9


RESULT   3
US-08-920-579-4
; Sequence 4, Application US/08920579
; GENERAL INFORMATION:
;   APPLICANT:  Fish, Eleanor N.
;   TITLE OF INVENTION:  Interferon Receptor Binding Peptide
;   NUMBER OF SEQUENCES:  17
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  BEREKSIN & PARR
;     STREET:  40 King Street West
;     CITY:  Toronto
;     STATE:  Ontario
;     COUNTRY:  Canada
;     ZIP:  M5H 3Y2
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/920,579
;     FILING DATE:  29-AUG-1997
;     CLASSIFICATION:  530
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Rudolph, John R.
;     REGISTRATION NUMBER:  38,003
;     REFERENCE/DOCKET NUMBER:  7841-92
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (416) 364-7311
;     TELEFAX:  (416) 361-1398
; INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  11 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-920-579-4


  Query Match             100.0%;  Score 42;  DB 13;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
Db       2 LTEKKYSP 9


RESULT   4
US-07-980-525-5
; Sequence 5, Application US/07980525
; GENERAL INFORMATION:
;   APPLICANT:  FISH, Eleanor N.
;   TITLE OF INVENTION:  INTERFERON RECEPTOR BINDING PEPTIDES
;   NUMBER OF SEQUENCES:  17
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram
;     STREET:  655 Fifteenth Street N.W. Suite 330
;     CITY:  Washington
;     STATE:  D.C.
;     COUNTRY:  U.S.A.
;     ZIP:  20005-5701
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/07/980,525
;     FILING DATE:  19921120
;     CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US/07/909,738
;     FILING DATE:  07-JUL-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Murray, Robert B.
;     REGISTRATION NUMBER:  22,980
;     REFERENCE/DOCKET NUMBER:  638-2005
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (202)638-5000
;     TELEFAX:  (202)638-4810
; INFORMATION FOR SEQ ID NO:  5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  18 amino acids
;     TYPE:  AMINO ACID
;     TOPOLOGY:  unknown
;   MOLECULE TYPE:  peptide
US-07-980-525-5


  Query Match             100.0%;  Score 42;  DB 3;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
```

```
Db      9 LTEKKYSP 16


RESULT   5
US-08-920-579-5
; Sequence 5, Application US/08920579
;  GENERAL INFORMATION:
;    APPLICANT:  Fish, Eleanor N.
;    TITLE OF INVENTION:  Interferon Receptor Binding Peptide
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BEREKSIN & PARR
;      STREET:  40 King Street West
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5H 3Y2
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/920,579
;      FILING DATE:  29-AUG-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rudolph, John R.
;      REGISTRATION NUMBER:  38,003
;      REFERENCE/DOCKET NUMBER:  7841-92
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 364-7311
;      TELEFAX:  (416) 361-1398
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-920-579-5


  Query Match             100.0%;  Score 42;  DB 13;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
Db       9 LTEKKYSP 16


RESULT   6
US-08-769-062-79
; Sequence 79, Application US/08769062
;  GENERAL INFORMATION:
;    APPLICANT:  Patten, Phillip
;    APPLICANT:  Stemmer, Willem
;    TITLE OF INVENTION:  Methods and compositions for
;    TITLE OF INVENTION:  polypeptide engineering
;    NUMBER OF SEQUENCES:  97
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Affymax Research Institute
;      STREET:  4001 Miranda Avenue
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94024
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/769,062
;      FILING DATE:  18-DEC-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/198,431
;      FILING DATE:  17-FEB-1994
;      APPLICATION NUMBER:  08/425,684
;      FILING DATE:  18-APR-1995
;      APPLICATION NUMBER:  08/537,874
;      FILING DATE:  30-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stevens, Lauren L
;      REGISTRATION NUMBER:  36,691
;      REFERENCE/DOCKET NUMBER:  2026
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-812-8803
;      TELEFAX:  415-424-0832
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  79:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-769-062-79


  Query Match             100.0%;  Score 42;  DB 11;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.36;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
Db      11 LTEKKYSP 18


RESULT   7
US-60-182-467-1317
; Sequence 1317, Application US/60182467
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION: USES THEREOF
;  FILE REFERENCE: CL000248
;  CURRENT APPLICATION NUMBER: US/60/182,467
;  CURRENT FILING DATE: 2000-02-15
;  NUMBER OF SEQ ID NOS: 2194
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1317
;   LENGTH: 46
;   TYPE: PRT
;   ORGANISM: HUMAN
US-60-182-467-1317


  Query Match             100.0%;  Score 42;  DB 24;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 0.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
Db      13 LTEKKYSP 20


RESULT   8
US-60-163-123-1406
; Sequence 1406, Application US/60163123
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
```

```
;  TITLE OF INVENTION: USES THEREOF
;  FILE REFERENCE: CL000137
;  CURRENT APPLICATION NUMBER: US/60/163,123
;  CURRENT FILING DATE: 1999-11-02
;  NUMBER OF SEQ ID NOS: 1986
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1406
;   LENGTH: 60
;   TYPE: PRT
;   ORGANISM: Human
US-60-163-123-1406


  Query Match             100.0%;  Score 42;  DB 24;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 0.83;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db      25 LTEKKYSP 32


RESULT   9
US-60-177-571-2851
; Sequence 2851, Application US/60177571
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: CL000201
;  CURRENT APPLICATION NUMBER: US/60/177,571
;  CURRENT FILING DATE: 2000-01-27
;  NUMBER OF SEQ ID NOS: 5082
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2851
;   LENGTH: 70
;   TYPE: PRT
;   ORGANISM: HUMAN
US-60-177-571-2851


  Query Match             100.0%;  Score 42;  DB 24;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 0.99;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db      39 LTEKKYSP 46


RESULT  10
US-60-177-571-2858
; Sequence 2858, Application US/60177571
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: CL000201
;  CURRENT APPLICATION NUMBER: US/60/177,571
;  CURRENT FILING DATE: 2000-01-27
;  NUMBER OF SEQ ID NOS: 5082
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2858
;   LENGTH: 71
;   TYPE: PRT
;   ORGANISM: HUMAN
US-60-177-571-2858


  Query Match             100.0%;  Score 42;  DB 24;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db      38 LTEKKYSP 45


RESULT  11
US-09-275-278-11
; Sequence 11, Application US/09275278
; GENERAL INFORMATION:
;  APPLICANT:  Ford, John
;  APPLICANT:  Yeung, George
;  APPLICANT:  Mulero, Julio
;  TITLE OF INVENTION:  A NOVEL INTERFERON AND USES THEREOF
;  FILE REFERENCE:  20411-772 (28110/36060)
;  CURRENT APPLICATION NUMBER: US/09/275,278
;  CURRENT FILING DATE:  1999-03-23
;  PRIOR APPLICATION NUMBER:  US 09/137,348
;  PRIOR FILING DATE:  1998-08-20
;  PRIOR APPLICATION NUMBER:  US 09/034,878
;  PRIOR FILING DATE:  1998-03-04
;  NUMBER OF SEQ ID NOS:  17
;  SOFTWARE:  FastSEQ for Windows Version 3.0            PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 72
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-275-278-11


  Query Match             100.0%;  Score 42;  DB 16;  Length 72;
  Best Local Similarity   100.0%;  Pred. No. 1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db      65 LTEKKYSP 72


RESULT  12
US-60-177-571-2852
; Sequence 2852, Application US/60177571
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: CL000201
;  CURRENT APPLICATION NUMBER: US/60/177,571
;  CURRENT FILING DATE: 2000-01-27
;  NUMBER OF SEQ ID NOS: 5082
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2852
;   LENGTH: 73
;   TYPE: PRT
;   ORGANISM: HUMAN
US-60-177-571-2852


  Query Match             100.0%;  Score 42;  DB 24;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db      38 LTEKKYSP 45


RESULT  13
US-60-177-571-2853
; Sequence 2853, Application US/60177571
; GENERAL INFORMATION:
```

```
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: CL000201
;  CURRENT APPLICATION NUMBER: US/60/177,571
;  CURRENT FILING DATE: 2000-01-27
;  NUMBER OF SEQ ID NOS: 5082
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2853
;   LENGTH: 73
;   TYPE: PRT
;   ORGANISM: HUMAN
US-60-177-571-2853


  Query Match           100.0%;  Score 42;  DB 24;  Length 73;
  Best Local Similarity  100.0%;  Pred. No. 1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db      38 LTEKKYSP 45


RESULT  14
US-60-177-571-2854
; Sequence 2854, Application US/60177571
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: CL000201
;  CURRENT APPLICATION NUMBER: US/60/177,571
;  CURRENT FILING DATE: 2000-01-27
;  NUMBER OF SEQ ID NOS: 5082
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2854
;   LENGTH: 73
;   TYPE: PRT
;   ORGANISM: HUMAN
US-60-177-571-2854


  Query Match           100.0%;  Score 42;  DB 24;  Length 73;
  Best Local Similarity  100.0%;  Pred. No. 1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db      38 LTEKKYSP 45


RESULT  15
US-60-177-571-2855
; Sequence 2855, Application US/60177571
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: CL000201
;  CURRENT APPLICATION NUMBER: US/60/177,571
;  CURRENT FILING DATE: 2000-01-27
;  NUMBER OF SEQ ID NOS: 5082
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2855
;   LENGTH: 73
;   TYPE: PRT
;   ORGANISM: HUMAN
US-60-177-571-2855


  Query Match           100.0%;  Score 42;  DB 24;  Length 73;
  Best Local Similarity  100.0%;  Pred. No. 1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db      38 LTEKKYSP 45


Search completed: December 13, 2001, 10:49:31
Job time: 291 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:44:40 ; Search time 9.21 Seconds
(without alignments)
10.008 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 61579 seqs, 11521160 residues

Total number of hits satisfying chosen parameters: 61579

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	8	5	US-09-424-080A-1	Sequence 1, Appli
2	42	100.0	166	5	US-09-977-034-2	Sequence 2, Appli
3	42	100.0	166	5	US-09-977-034-8	Sequence 8, Appli
4	42	100.0	166	5	US-09-977-034-10	Sequence 10, Appl
5	42	100.0	166	5	US-09-977-034-11	Sequence 11, Appl
6	42	100.0	166	5	US-09-977-034-12	Sequence 12, Appl
7	42	100.0	166	5	US-09-977-034-18	Sequence 18, Appl
8	42	100.0	166	5	US-09-977-034-19	Sequence 19, Appl
9	36	85.7	165	5	US-09-633-516B-13	Sequence 13, Appl
10	36	85.7	165	5	US-09-633-516B-14	Sequence 14, Appl
11	36	85.7	165	5	US-09-977-034-9	Sequence 9, Appli
12	36	85.7	166	5	US-09-977-034-13	Sequence 13, Appl
13	36	85.7	170	5	US-09-977-034-16	Sequence 16, Appl
14	36	85.7	831	6	US-60-329-756-2	Sequence 2, Appli
15	35	83.3	166	5	US-09-977-034-14	Sequence 14, Appl
16	33	78.6	166	5	US-09-977-034-15	Sequence 15, Appl
17	31	73.8	166	5	US-09-977-034-22	Sequence 22, Appl
18	31	73.8	166	5	US-09-977-034-25	Sequence 25, Appl
19	31	73.8	166	5	US-09-977-034-26	Sequence 26, Appl
20	31	73.8	166	5	US-09-977-034-28	Sequence 28, Appl
21	31	73.8	167	5	US-09-977-034-23	Sequence 23, Appl
22	31	73.8	167	5	US-09-977-034-27	Sequence 27, Appl
23	31	73.8	167	5	US-09-977-034-29	Sequence 29, Appl
24	31	73.8	198	5	US-09-823-307-2	Sequence 2, Appli
25	31	73.8	198	5	US-09-972-524-2	Sequence 2, Appli
26	31	73.8	198	5	US-09-823-307A-2	Sequence 2, Appli
27	31	73.8	427	5	US-09-897-516-7860	Sequence 7860, Ap
28	31	73.8	549	5	US-09-550-115A-7	Sequence 7, Appli
29	30	71.4	245	5	US-09-897-516-4514	Sequence 4514, Ap
30	30	71.4	415	5	US-09-976-059-20	Sequence 20, Appl
31	30	71.4	518	5	US-09-625-972-23	Sequence 23, Appl
32	29	69.0	119	5	US-09-550-115A-1	Sequence 1, Appli
33	29	69.0	123	5	US-09-550-115A-3	Sequence 3, Appli
34	29	69.0	166	5	US-09-977-034-17	Sequence 17, Appl
35	29	69.0	172	5	US-09-977-034-21	Sequence 21, Appl
36	29	69.0	178	5	US-09-927-850-6	Sequence 6, Appli
37	29	69.0	179	5	US-09-927-850-13	Sequence 13, Appl
38	29	69.0	179	5	US-09-927-850-15	Sequence 15, Appl
39	29	69.0	182	5	US-09-927-850-17	Sequence 17, Appl
40	29	69.0	207	5	US-09-927-850-5	Sequence 5, Appli
41	29	69.0	418	5	US-09-550-115A-10	Sequence 10, Appl
42	29	69.0	502	5	US-09-815-242-10425	Sequence 10425, A
43	29	69.0	532	5	US-09-897-516-8145	Sequence 8145, Ap
44	29	69.0	559	5	US-09-550-115A-5	Sequence 5, Appli
45	29	69.0	559	5	US-09-550-115A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-424-080A-1
; Sequence 1, Application US/09424080A
; GENERAL INFORMATION:
; APPLICANT: ZAVIALOV, Vladimir et al.
; TITLE OF INVENTION: COMPOSITION FOR ENHANCING IMMUNOSUPPRESANTS PHARMACEUTICAL ACT
; FILE REFERENCE: 0933-0149P
; CURRENT APPLICATION NUMBER: US/09/424,080A
; CURRENT FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide corresponding to the high-affinity binding/anti-
; OTHER INFORMATION: lymphoproliferative
; OTHER INFORMATION: site of human IFN-alpha
US-09-424-080A-1

Query Match 100.0%; Score 42; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.4e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 LTEKKYSP 8
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Db      1 LTEKKYSP 8
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RESULT 2
US-09-977-034-2
; Sequence 2, Application US/09977034
; GENERAL INFORMATION:
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Sun, Yaping
; APPLICANT: Gillies, Stephen D.
; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as
; TITLE OF INVENTION: Fc Fusion Proteins
; FILE REFERENCE: LEX-009
; CURRENT APPLICATION NUMBER: US/09/977,034
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US/09/575,503
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/134,895
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

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;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-977-034-2


  Query Match           100.0%;  Score 42;  DB 5;  Length 166;
  Best Local Similarity  100.0%;  Pred. No. 0.067;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    131 LTEKKYSP 138


RESULT   3
US-09-977-034-8
; Sequence 8, Application US/09977034
; GENERAL INFORMATION:
;  APPLICANT: Lo, Kin-Ming
;  APPLICANT:  Sun, Yaping
;  APPLICANT:  Gillies, Stephen D.
;  TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as
;  TITLE OF INVENTION:  Fc Fusion Proteins
;  FILE REFERENCE: LEX-009
;  CURRENT APPLICATION NUMBER: US/09/977,034
;  CURRENT FILING DATE:  2001-10-11
;  PRIOR APPLICATION NUMBER: US/09/575,503
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 60/134,895
;  PRIOR FILING DATE: 1999-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human IFN alpha-1 protein
US-09-977-034-8


  Query Match           100.0%;  Score 42;  DB 5;  Length 166;
  Best Local Similarity  100.0%;  Pred. No. 0.067;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    131 LTEKKYSP 138


RESULT   4
US-09-977-034-10
; Sequence 10, Application US/09977034
; GENERAL INFORMATION:
;  APPLICANT: Lo, Kin-Ming
;  APPLICANT:  Sun, Yaping
;  APPLICANT:  Gillies, Stephen D.
;  TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as
;  TITLE OF INVENTION:  Fc Fusion Proteins
;  FILE REFERENCE: LEX-009
;  CURRENT APPLICATION NUMBER: US/09/977,034
;  CURRENT FILING DATE:  2001-10-11
;  PRIOR APPLICATION NUMBER: US/09/575,503
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 60/134,895
;  PRIOR FILING DATE: 1999-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human IFN alpha-4 protein
US-09-977-034-10


  Query Match           100.0%;  Score 42;  DB 5;  Length 166;
  Best Local Similarity  100.0%;  Pred. No. 0.067;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    131 LTEKKYSP 138


RESULT   5
US-09-977-034-11
; Sequence 11, Application US/09977034
; GENERAL INFORMATION:
;  APPLICANT: Lo, Kin-Ming
;  APPLICANT:  Sun, Yaping
;  APPLICANT:  Gillies, Stephen D.
;  TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as
;  TITLE OF INVENTION:  Fc Fusion Proteins
;  FILE REFERENCE: LEX-009
;  CURRENT APPLICATION NUMBER: US/09/977,034
;  CURRENT FILING DATE:  2001-10-11
;  PRIOR APPLICATION NUMBER: US/09/575,503
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 60/134,895
;  PRIOR FILING DATE: 1999-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human IFN alpha-5 protein
US-09-977-034-11


  Query Match           100.0%;  Score 42;  DB 5;  Length 166;
  Best Local Similarity  100.0%;  Pred. No. 0.067;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    131 LTEKKYSP 138


RESULT   6
US-09-977-034-12
; Sequence 12, Application US/09977034
; GENERAL INFORMATION:
;  APPLICANT: Lo, Kin-Ming
;  APPLICANT:  Sun, Yaping
;  APPLICANT:  Gillies, Stephen D.
;  TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as
;  TITLE OF INVENTION:  Fc Fusion Proteins
;  FILE REFERENCE: LEX-009
;  CURRENT APPLICATION NUMBER: US/09/977,034
;  CURRENT FILING DATE:  2001-10-11
;  PRIOR APPLICATION NUMBER: US/09/575,503
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 60/134,895
;  PRIOR FILING DATE: 1999-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
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; OTHER INFORMATION: HUman IFN alpha-6 protein
US-09-977-034-12

Query Match 100.0%; Score 42; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 131 LTEKKYSP 138

RESULT 7
US-09-977-034-18
; Sequence 18, Application US/09977034
; GENERAL INFORMATION:
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Sun, Yaping
; APPLICANT: Gillies, Stephen D.
; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as
; TITLE OF INVENTION: Fc Fusion Proteins
; FILE REFERENCE: LEX-009
; CURRENT APPLICATION NUMBER: US/09/977,034
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US/09/575,503
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/134,895
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human IFN alpha-17 protein
US-09-977-034-18

Query Match 100.0%; Score 42; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 131 LTEKKYSP 138

RESULT 8
US-09-977-034-19
; Sequence 19, Application US/09977034
; GENERAL INFORMATION:
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Sun, Yaping
; APPLICANT: Gillies, Stephen D.
; TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as
; TITLE OF INVENTION: Fc Fusion Proteins
; FILE REFERENCE: LEX-009
; CURRENT APPLICATION NUMBER: US/09/977,034
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US/09/575,503
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/134,895
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human IFN alpha-21 protein
US-09-977-034-19

Query Match 100.0%; Score 42; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
||||||||
Db 131 LTEKKYSP 138

RESULT 9
US-09-633-516B-13
; Sequence 13, Application US/09633516B
; GENERAL INFORMATION:
; APPLICANT: Francis Joseph CARR
; APPLICANT: Fiona Suzanne ADAIR
; APPLICANT: Anita Anne HAMILTON
; APPLICANT: Graham CARTER
; TITLE OF INVENTION: Modifying Protein Immunogenicity
; FILE REFERENCE: 112408-120
; CURRENT APPLICATION NUMBER: US/09/633,516B
; 2000-08-04
; CURRENT FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: PCT/GB99/04119
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: GB9826925.1
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: GB9902139.6
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-633-516B-13

Query Match 85.7%; Score 36; DB 5; Length 165;
Best Local Similarity 87.5%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LTEKKYSP 8
| ||||||
Db 130 LKEKKYSP 137

RESULT 10
US-09-633-516B-14
; Sequence 14, Application US/09633516B
; GENERAL INFORMATION:
; APPLICANT: Francis Joseph CARR
; APPLICANT: Fiona Suzanne ADAIR
; APPLICANT: Anita Anne HAMILTON
; APPLICANT: Graham CARTER
; TITLE OF INVENTION: Modifying Protein Immunogenicity
; FILE REFERENCE: 112408-120
; CURRENT APPLICATION NUMBER: US/09/633,516B
; 2000-08-04
; CURRENT FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: PCT/GB99/04119
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: GB9826925.1
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: GB9902139.6
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 165
; TYPE: PRT

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;   ORGANISM: Homo sapiens
US-09-633-516B-14


  Query Match             85.7%;  Score 36;  DB 5;  Length 165;
  Best Local Similarity   87.5%;  Pred. No. 1.1;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
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Db     130 LKEKKYSP 137


RESULT  11
US-09-977-034-9
; Sequence 9, Application US/09977034
; GENERAL INFORMATION:
;  APPLICANT: Lo, Kin-Ming
;  APPLICANT:  Sun, Yaping
;  APPLICANT:  Gillies, Stephen D.
;  TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as
;  TITLE OF INVENTION:  Fc Fusion Proteins
;  FILE REFERENCE: LEX-009
;  CURRENT APPLICATION NUMBER: US/09/977,034
;  CURRENT FILING DATE:  2001-10-11
;  PRIOR APPLICATION NUMBER: US/09/575,503
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 60/134,895
;  PRIOR FILING DATE: 1999-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 165
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human IFN alpha-2 protein
US-09-977-034-9


  Query Match             85.7%;  Score 36;  DB 5;  Length 165;
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  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            | ||||||
Db     130 LKEKKYSP 137


RESULT  12
US-09-977-034-13
; Sequence 13, Application US/09977034
; GENERAL INFORMATION:
;  APPLICANT: Lo, Kin-Ming
;  APPLICANT:  Sun, Yaping
;  APPLICANT:  Gillies, Stephen D.
;  TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as
;  TITLE OF INVENTION:  Fc Fusion Proteins
;  FILE REFERENCE: LEX-009
;  CURRENT APPLICATION NUMBER: US/09/977,034
;  CURRENT FILING DATE:  2001-10-11
;  PRIOR APPLICATION NUMBER: US/09/575,503
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 60/134,895
;  PRIOR FILING DATE: 1999-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human IFN alpha-7 protein
US-09-977-034-13


  Query Match             85.7%;  Score 36;  DB 5;  Length 166;
  Best Local Similarity   87.5%;  Pred. No. 1.1;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            | ||||||
Db     131 LMEKKYSP 138


RESULT  13
US-09-977-034-16
; Sequence 16, Application US/09977034
; GENERAL INFORMATION:
;  APPLICANT: Lo, Kin-Ming
;  APPLICANT:  Sun, Yaping
;  APPLICANT:  Gillies, Stephen D.
;  TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as
;  TITLE OF INVENTION:  Fc Fusion Proteins
;  FILE REFERENCE: LEX-009
;  CURRENT APPLICATION NUMBER: US/09/977,034
;  CURRENT FILING DATE:  2001-10-11
;  PRIOR APPLICATION NUMBER: US/09/575,503
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 60/134,895
;  PRIOR FILING DATE: 1999-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human IFN alpha-14 protein
US-09-977-034-16


  Query Match             85.7%;  Score 36;  DB 5;  Length 170;
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  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            | ||||||
Db     135 LMEKKYSP 142


RESULT  14
US-60-329-756-2
; Sequence 2, Application US/60329756
; GENERAL INFORMATION:
;  APPLICANT: COR Therapeutics, Inc.
;  APPLICANT:  Tomlinson, James E.
;  TITLE OF INVENTION: VELP2 Gene and Protein
;  FILE REFERENCE: 044481-5087-PR
;  CURRENT APPLICATION NUMBER: US/60/329,756
;  CURRENT FILING DATE:  2001-10-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 831
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-329-756-2


  Query Match             85.7%;  Score 36;  DB 6;  Length 831;
  Best Local Similarity   75.0%;  Pred. No. 6;
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Qy       1 LTEKKYSP 8
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Db      690 VTERKYSP 697


RESULT  15
US-09-977-034-14
; Sequence 14, Application US/09977034
; GENERAL INFORMATION:
;  APPLICANT: Lo, Kin-Ming
;  APPLICANT:  Sun, Yaping
;  APPLICANT:  Gillies, Stephen D.
;  TITLE OF INVENTION: Expression and Export of Interferon-Alpha Proteins as
;  TITLE OF INVENTION:  Fc Fusion Proteins
;  FILE REFERENCE: LEX-009
;  CURRENT APPLICATION NUMBER: US/09/977,034
;  CURRENT FILING DATE:  2001-10-11
;  PRIOR APPLICATION NUMBER: US/09/575,503
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 60/134,895
;  PRIOR FILING DATE: 1999-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human IFN alpha-8 protein
US-09-977-034-14


  Query Match           83.3%;  Score 35;  DB 5;  Length 166;
  Best Local Similarity  100.0%;  Pred. No. 1.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYS 7
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Db     131 LTEKKYS 137


Search completed: December 13, 2001, 10:49:47
Job time: 307 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:44:40 ; Search time 19.94 Seconds
(without alignments)
9.028 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	8	2	US-08-669-284B-30	Sequence 30, Appl
2	42	100.0	11	1	US-08-362-453-4	Sequence 4, Appli
3	42	100.0	18	1	US-08-362-453-5	Sequence 5, Appli
4	42	100.0	150	1	US-08-362-453-10	Sequence 10, Appl
5	42	100.0	150	1	US-08-362-453-11	Sequence 11, Appl
6	42	100.0	150	1	US-08-362-453-12	Sequence 12, Appl
7	42	100.0	162	1	US-08-362-453-15	Sequence 15, Appl
8	42	100.0	165	1	US-08-362-453-13	Sequence 13, Appl
9	42	100.0	165	1	US-08-362-453-14	Sequence 14, Appl
10	42	100.0	166	1	US-08-362-453-8	Sequence 8, Appli
11	42	100.0	166	1	US-08-362-453-9	Sequence 9, Appli
12	42	100.0	166	2	US-08-489-066A-16	Sequence 16, Appl
13	42	100.0	166	3	US-08-489-072A-16	Sequence 16, Appl
14	42	100.0	166	3	US-08-819-238A-2	Sequence 2, Appli
15	42	100.0	166	4	US-08-954-395A-9	Sequence 9, Appli
16	42	100.0	166	4	US-08-954-395A-10	Sequence 10, Appl
17	42	100.0	166	4	US-08-954-395A-11	Sequence 11, Appl
18	42	100.0	166	4	US-08-954-395A-12	Sequence 12, Appl
19	42	100.0	166	4	US-08-954-395A-13	Sequence 13, Appl
20	42	100.0	166	4	US-08-954-395A-14	Sequence 14, Appl
21	42	100.0	166	4	US-08-954-395A-15	Sequence 15, Appl
22	42	100.0	166	4	US-08-954-395A-16	Sequence 16, Appl
23	42	100.0	166	4	US-08-954-395A-17	Sequence 17, Appl
24	42	100.0	166	4	US-08-489-071A-16	Sequence 16, Appl
25	42	100.0	166	4	US-09-339-913B-75	Sequence 75, Appl
26	42	100.0	166	4	US-09-339-913B-76	Sequence 76, Appl
27	42	100.0	166	4	US-09-339-913B-77	Sequence 77, Appl
28	42	100.0	166	4	US-09-339-913B-79	Sequence 79, Appl
29	42	100.0	166	4	US-09-339-913B-80	Sequence 80, Appl
30	42	100.0	166	4	US-09-339-913B-83	Sequence 83, Appl
31	42	100.0	166	4	US-09-339-913B-84	Sequence 84, Appl
32	42	100.0	166	4	US-09-339-913B-85	Sequence 85, Appl
33	42	100.0	189	1	US-08-026-758-1	Sequence 1, Appli
34	42	100.0	189	1	US-08-026-758-2	Sequence 2, Appli
35	42	100.0	189	1	US-08-026-758-3	Sequence 3, Appli
36	42	100.0	189	1	US-08-026-758-6	Sequence 6, Appli
37	42	100.0	189	1	US-08-026-758-7	Sequence 7, Appli
38	42	100.0	189	1	US-08-026-758-11	Sequence 11, Appl
39	42	100.0	189	1	US-08-026-758-16	Sequence 16, Appl
40	42	100.0	189	1	US-08-026-758-17	Sequence 17, Appl
41	42	100.0	189	1	US-08-026-758-19	Sequence 19, Appl
42	42	100.0	189	1	US-08-026-758-20	Sequence 20, Appl
43	42	100.0	189	2	US-08-489-066A-2	Sequence 2, Appli
44	42	100.0	189	3	US-08-489-072A-2	Sequence 2, Appli
45	42	100.0	189	4	US-09-206-935-8	Sequence 8, Appli

ALIGNMENTS

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RESULT 1
US-08-669-284B-30
; Sequence 30, Application US/08669284B
; Patent No. 5939534
;  GENERAL INFORMATION:
;    APPLICANT:  Inoue, Makoto
;    APPLICANT:  Kikuchi, Kaoru
;    APPLICANT:  Ishige, Yoko
;    APPLICANT:  Ito, Akira
;    APPLICANT:  Kimura, Toru
;    APPLICANT:  Nakayama, Chikao
;    APPLICANT:  No. 5939534uchi, Hiroshi
;    TITLE OF INVENTION:  NOVEL HUMAN CILIARY NEUROTROPHIC FACTORS
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/669,284B
;      FILING DATE:  28-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP94/02269
;      FILING DATE:  27-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 06-268281
;      FILING DATE:  05-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 06-201504
;      FILING DATE:  02-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 05-350934
;      FILING DATE:  29-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nakamura, Dean H.
;      REGISTRATION NUMBER:  33,981
;      REFERENCE/DOCKET NUMBER:  Q-42041
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)293-7060
;      TELEFAX:  (202)293-7860
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
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;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-669-284B-30


  Query Match             100.0%;  Score 42;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
Db       1 LTEKKYSP 8


RESULT   2
US-08-362-453-4
; Sequence 4, Application US/08362453
; Patent No. 5684129
;  GENERAL INFORMATION:
;    APPLICANT:  FISH, Eleanor N.
;    TITLE OF INVENTION:  INTERFERON RECEPTOR BINDING PEPTIDES
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/362,453
;      FILING DATE:  06-JAN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/909,739
;      APPLICATION NUMBER:  FILING DATE: 07-JUL-1992
;      APPLICATION NUMBER:  US 07/980,525
;      APPLICATION NUMBER:  FILING DATE: 20-NOV-1992
;      APPLICATION NUMBER:  PCT/CA93/00279
;      APPLICATION NUMBER:  FILING DATE: 06-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitts, Monica Chin
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P638-4017
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-5000
;      TELEFAX:  (202) 638-4810
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-362-453-4


  Query Match             100.0%;  Score 42;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0064;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
Db       2 LTEKKYSP 9


RESULT   3
US-08-362-453-5
; Sequence 5, Application US/08362453
; Patent No. 5684129
;  GENERAL INFORMATION:
;    APPLICANT:  FISH, Eleanor N.
;    TITLE OF INVENTION:  INTERFERON RECEPTOR BINDING PEPTIDES
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/362,453
;      FILING DATE:  06-JAN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/909,739
;      APPLICATION NUMBER:  FILING DATE: 07-JUL-1992
;      APPLICATION NUMBER:  US 07/980,525
;      APPLICATION NUMBER:  FILING DATE: 20-NOV-1992
;      APPLICATION NUMBER:  PCT/CA93/00279
;      APPLICATION NUMBER:  FILING DATE: 06-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitts, Monica Chin
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P638-4017
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-5000
;      TELEFAX:  (202) 638-4810
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-362-453-5


  Query Match             100.0%;  Score 42;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
Db       9 LTEKKYSP 16


RESULT   4
US-08-362-453-10
; Sequence 10, Application US/08362453
; Patent No. 5684129
;  GENERAL INFORMATION:
;    APPLICANT:  FISH, Eleanor N.
;    TITLE OF INVENTION:  INTERFERON RECEPTOR BINDING PEPTIDES
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/362,453
;       FILING DATE:  06-JAN-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/909,739
;       APPLICATION NUMBER:  FILING DATE: 07-JUL-1992
;       APPLICATION NUMBER:  US 07/980,525
;       APPLICATION NUMBER:  FILING DATE: 20-NOV-1992
;       APPLICATION NUMBER:  PCT/CA93/00279
;       APPLICATION NUMBER:  FILING DATE: 06-JUL-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kitts, Monica Chin
;       REGISTRATION NUMBER:  36,105
;       REFERENCE/DOCKET NUMBER:  P638-4017
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 638-5000
;       TELEFAX:  (202) 638-4810
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  150 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  protein
US-08-362-453-10


  Query Match             100.0%;  Score 42;  DB 1;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
Db     126 LTEKKYSP 133


RESULT   5
US-08-362-453-11
; Sequence 11, Application US/08362453
; Patent No. 5684129
;  GENERAL INFORMATION:
;    APPLICANT:  FISH, Eleanor N.
;    TITLE OF INVENTION:  INTERFERON RECEPTOR BINDING PEPTIDES
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/362,453
;      FILING DATE:  06-JAN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/909,739
;      APPLICATION NUMBER:  FILING DATE: 07-JUL-1992
;      APPLICATION NUMBER:  US 07/980,525
;      APPLICATION NUMBER:  FILING DATE: 20-NOV-1992
;      APPLICATION NUMBER:  PCT/CA93/00279
;      APPLICATION NUMBER:  FILING DATE: 06-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitts, Monica Chin
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P638-4017
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-5000
;      TELEFAX:  (202) 638-4810
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  150 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-362-453-11


  Query Match             100.0%;  Score 42;  DB 1;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
Db     126 LTEKKYSP 133


RESULT   6
US-08-362-453-12
; Sequence 12, Application US/08362453
; Patent No. 5684129
;  GENERAL INFORMATION:
;    APPLICANT:  FISH, Eleanor N.
;    TITLE OF INVENTION:  INTERFERON RECEPTOR BINDING PEPTIDES
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/362,453
;      FILING DATE:  06-JAN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/909,739
;      APPLICATION NUMBER:  FILING DATE: 07-JUL-1992
;      APPLICATION NUMBER:  US 07/980,525
;      APPLICATION NUMBER:  FILING DATE: 20-NOV-1992
;      APPLICATION NUMBER:  PCT/CA93/00279
;      APPLICATION NUMBER:  FILING DATE: 06-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitts, Monica Chin
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P638-4017
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-5000
;      TELEFAX:  (202) 638-4810
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  150 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-362-453-12


  Query Match             100.0%;  Score 42;  DB 1;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 LTEKKYSP 8
          ||||||||
Db    126 LTEKKYSP 133


RESULT   7
US-08-362-453-15
; Sequence 15, Application US/08362453
; Patent No. 5684129
;  GENERAL INFORMATION:
;    APPLICANT:  FISH, Eleanor N.
;    TITLE OF INVENTION:  INTERFERON RECEPTOR BINDING PEPTIDES
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/362,453
;      FILING DATE:  06-JAN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/909,739
;      APPLICATION NUMBER:  FILING DATE: 07-JUL-1992
;      APPLICATION NUMBER:  US 07/980,525
;      APPLICATION NUMBER:  FILING DATE: 20-NOV-1992
;      APPLICATION NUMBER:  PCT/CA93/00279
;      APPLICATION NUMBER:  FILING DATE: 06-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitts, Monica Chin
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P638-4017
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-5000
;      TELEFAX:  (202) 638-4810
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  162 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-362-453-15


  Query Match           100.0%;  Score 42;  DB 1;  Length 162;
  Best Local Similarity  100.0%;  Pred. No. 0.12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    127 LTEKKYSP 134


RESULT   8
US-08-362-453-13
; Sequence 13, Application US/08362453
; Patent No. 5684129
;  GENERAL INFORMATION:
;    APPLICANT:  FISH, Eleanor N.
;    TITLE OF INVENTION:  INTERFERON RECEPTOR BINDING PEPTIDES
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/362,453
;      FILING DATE:  06-JAN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/909,739
;      APPLICATION NUMBER:  FILING DATE: 07-JUL-1992
;      APPLICATION NUMBER:  US 07/980,525
;      APPLICATION NUMBER:  FILING DATE: 20-NOV-1992
;      APPLICATION NUMBER:  PCT/CA93/00279
;      APPLICATION NUMBER:  FILING DATE: 06-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitts, Monica Chin
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P638-4017
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-5000
;      TELEFAX:  (202) 638-4810
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  165 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-362-453-13


  Query Match           100.0%;  Score 42;  DB 1;  Length 165;
  Best Local Similarity  100.0%;  Pred. No. 0.12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 LTEKKYSP 8
          ||||||||
Db    130 LTEKKYSP 137


RESULT   9
US-08-362-453-14
; Sequence 14, Application US/08362453
; Patent No. 5684129
;  GENERAL INFORMATION:
;    APPLICANT:  FISH, Eleanor N.
;    TITLE OF INVENTION:  INTERFERON RECEPTOR BINDING PEPTIDES
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/362,453
;      FILING DATE:  06-JAN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/909,739
;      APPLICATION NUMBER:  FILING DATE: 07-JUL-1992
;      APPLICATION NUMBER:  US 07/980,525
;      APPLICATION NUMBER:  FILING DATE: 20-NOV-1992
```

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;       APPLICATION NUMBER:  PCT/CA93/00279
;       APPLICATION NUMBER:  FILING DATE: 06-JUL-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kitts, Monica Chin
;       REGISTRATION NUMBER:  36,105
;       REFERENCE/DOCKET NUMBER:  P638-4017
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 638-5000
;       TELEFAX:  (202) 638-4810
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  165 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  protein
US-08-362-453-14


  Query Match           100.0%;  Score 42;  DB 1;  Length 165;
  Best Local Similarity  100.0%;  Pred. No. 0.12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
Db     130 LTEKKYSP 137


RESULT  10
US-08-362-453-8
; Sequence 8, Application US/08362453
; Patent No. 5684129
;  GENERAL INFORMATION:
;    APPLICANT:  FISH, Eleanor N.
;    TITLE OF INVENTION:  INTERFERON RECEPTOR BINDING PEPTIDES
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/362,453
;      FILING DATE:  06-JAN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/909,739
;      APPLICATION NUMBER:  FILING DATE: 07-JUL-1992
;      APPLICATION NUMBER:  US 07/980,525
;      APPLICATION NUMBER:  FILING DATE: 20-NOV-1992
;      APPLICATION NUMBER:  PCT/CA93/00279
;      APPLICATION NUMBER:  FILING DATE: 06-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitts, Monica Chin
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P638-4017
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-5000
;      TELEFAX:  (202) 638-4810
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  166 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-362-453-8


  Query Match           100.0%;  Score 42;  DB 1;  Length 166;
  Best Local Similarity  100.0%;  Pred. No. 0.12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
Db     131 LTEKKYSP 138


RESULT  11
US-08-362-453-9
; Sequence 9, Application US/08362453
; Patent No. 5684129
;  GENERAL INFORMATION:
;    APPLICANT:  FISH, Eleanor N.
;    TITLE OF INVENTION:  INTERFERON RECEPTOR BINDING PEPTIDES
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/362,453
;      FILING DATE:  06-JAN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/909,739
;      APPLICATION NUMBER:  FILING DATE: 07-JUL-1992
;      APPLICATION NUMBER:  US 07/980,525
;      APPLICATION NUMBER:  FILING DATE: 20-NOV-1992
;      APPLICATION NUMBER:  PCT/CA93/00279
;      APPLICATION NUMBER:  FILING DATE: 06-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitts, Monica Chin
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P638-4017
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-5000
;      TELEFAX:  (202) 638-4810
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  166 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-362-453-9


  Query Match           100.0%;  Score 42;  DB 1;  Length 166;
  Best Local Similarity  100.0%;  Pred. No. 0.12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
           ||||||||
Db     131 LTEKKYSP 138


RESULT  12
US-08-489-066A-16
; Sequence 16, Application US/08489066A
; Patent No. 5869293
;  GENERAL INFORMATION:
;    APPLICANT:  PESTKA, SIDNEY
;    TITLE OF INVENTION:  SUPER PROTEINS INCLUDING INTERFERONS,
```

```
;    TITLE OF INVENTION:  INTERLEUKINS, ET AL.
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/489,066A
;      FILING DATE:  09-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/257,784
;      FILING DATE:  10-JUN-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/076,231
;      FILING DATE:  11-JUN-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fehlner, Ph.D., Esq., Paul F.
;      REGISTRATION NUMBER:  35,135
;      REFERENCE/DOCKET NUMBER:  1705-1-002 CIPC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201 343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  166 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  Hu-IFN-alpha001
US-08-489-066A-16


  Query Match             100.0%;  Score 42;  DB 2;  Length 166;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db     131 LTEKKYSP 138


RESULT  13
US-08-489-072A-16
; Sequence 16, Application US/08489072A
; Patent No. 6001589
;  GENERAL INFORMATION:
;    APPLICANT:  PESTKA, SIDNEY
;    TITLE OF INVENTION:  SUPER PROTEINS INCLUDING INTERFERONS,
;    TITLE OF INVENTION:  INTERLEUKINS, ET AL.
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/489,072A
;      FILING DATE:  09-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/257,784
;      FILING DATE:  10-JUN-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/076,231
;      FILING DATE:  11-JUN-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fehlner, Ph.D., Esq., Paul F.
;      REGISTRATION NUMBER:  35,135
;      REFERENCE/DOCKET NUMBER:  1705-1-002 CIPA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201 343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  166 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  Hu-IFN-alpha001
US-08-489-072A-16


  Query Match             100.0%;  Score 42;  DB 3;  Length 166;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db     131 LTEKKYSP 138


RESULT  14
US-08-819-238A-2
; Sequence 2, Application US/08819238A
; Patent No. 6069133
;  GENERAL INFORMATION:
;    APPLICANT:  Henry C. Chiou and Dennis J. Carlo
;    TITLE OF INVENTION:  TARGETED DELIVERY OF GENES ENCODING
;    TITLE OF INVENTION:  INTERFERON
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,238A
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/616,023
;      FILING DATE:  14 MARCH 1996
;      APPLICATION NUMBER:  PCT/US96/
```

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;       FILING DATE:  14 MARCH 1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  REMILLARD, JANE E.
;       REGISTRATION NUMBER:  38,872
;       REFERENCE/DOCKET NUMBER:  TTI-143CPPC
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)227-5941
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  166 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FRAGMENT TYPE:  internal
US-08-819-238A-2


  Query Match           100.0%;  Score 42;  DB 3;  Length 166;
  Best Local Similarity  100.0%;  Pred. No. 0.12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db     131 LTEKKYSP 138


RESULT  15
US-08-954-395A-9
; Sequence 9, Application US/08954395A
; Patent No. 6204022
;  GENERAL INFORMATION:
;    APPLICANT:  Johnson, Howard M.
;    APPLICANT:  Subramaniam, Prem S.
;    APPLICANT:  Pontzer, Carol H.
;    APPLICANT:  Villarete, Lorelie H.
;    APPLICANT:  Campos, Jackeline
;    APPLICANT:  Chung, Albert D.
;    APPLICANT:  Li, Wayne W.
;    APPLICANT:  Liu, Philip T.
;    TITLE OF INVENTION:  LOW-TOXICITY HUMAN INTERFERON-ALPHA
;    TITLE OF INVENTION:  ANALOG
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates  LLP
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/954,395A
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/631,328
;      FILING DATE:  12-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dehlinger, Peter J
;      REGISTRATION NUMBER:  27008
;      REFERENCE/DOCKET NUMBER:  5600-0001.35
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-324-0880
;      TELEFAX:  650-324-0960
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  166 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank Accessn. J00210, PID g386796
;      CLONE:  Human IFN alpha-d, mature protein
US-08-954-395A-9


  Query Match           100.0%;  Score 42;  DB 4;  Length 166;
  Best Local Similarity  100.0%;  Pred. No. 0.12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKKYSP 8
            ||||||||
Db     131 LTEKKYSP 138


Search completed: December 13, 2001, 10:45:08
Job time: 28 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 11:55:37 ; Search time 22.27 Seconds
(without alignments)
27.364 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 147

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	50.0	8	2	S21663	neuropeptide - flo
2	18	42.9	8	2	S15422	adipokinetic hormo
3	18	42.9	8	2	A58641	adipokinetic hormo
4	17	40.5	8	2	A05169	neuropeptide M-I -
5	16	38.1	8	2	S20162	leghemoglobin III
6	16	38.1	8	2	A14683	aspartate transami
7	16	38.1	8	2	S45651	probable Na+-trans
8	14	33.3	8	2	A61348	red pigment-concen
9	14	33.3	8	2	S08995	hypertrehalosemic
10	14	33.3	8	2	A49823	adipokinetic hormo
11	14	33.3	8	2	A44960	neuropeptide Led-C
12	14	33.3	8	2	A43976	hypertrehalosemic
13	14	33.3	8	2	B43976	hypertrehalosemic
14	14	33.3	8	2	S11545	adipokinetic hormo
15	14	33.3	8	2	D47393	neuropeptide calla
16	12	28.6	8	2	S16324	hypothetical prote
17	12	28.6	8	2	A23967	leucopyrokinin - M
18	11	26.2	8	2	S08996	hypertrehalosemic
19	11	26.2	8	2	S10596	adipokinetic hormo
20	11	26.2	8	2	B49823	adipokinetic hormo
21	11	26.2	8	2	B44960	neuropeptide Led-C
22	11	26.2	8	2	A33995	adipokinetic hormo
23	11	26.2	8	2	S55310	adipokinetic hormo
24	11	26.2	8	2	A58620	adipokinetic hormo
25	11	26.2	8	2	S21273	cellulase (EC 3.2.
26	11	26.2	8	2	S21288	lectin - potato (f
27	11	26.2	8	2	JS0318	leucokinin VIII -
28	11	26.2	8	2	I57018	gene Cftr protein
29	10	23.8	8	2	A32523	peptidyl-dipeptida
30	10	23.8	8	2	B24749	neuropeptide B - b
31	10	23.8	8	2	S63493	dissimilatory sulf
32	10	23.8	8	2	A41117	acetylcholinestera
33	10	23.8	8	2	I48935	apolipoprotein A-I
34	10	23.8	8	2	A35180	neutral proteinase
35	9	21.4	8	2	A31570	angiotensin-conver
36	9	21.4	8	2	PC1002	leucine--tRNA liga
37	9	21.4	8	2	T10952	hypothetical prote
38	9	21.4	8	2	T14906	hypothetical prote
39	9	21.4	8	2	PT0030	inulinase (EC 3.2.
40	9	21.4	8	2	S13661	polygalacturonase
41	9	21.4	8	2	A42057	fibroblast growth
42	9	21.4	8	2	A54823	olfactory receptor
43	9	21.4	8	2	B54823	olfactory receptor
44	9	21.4	8	2	I64832	Ca2+-transporting
45	9	21.4	8	2	A47618	beta-galactosidase

ALIGNMENTS

RESULT 1
S21663
neuropeptide - flower beetle (Pachnoda marginata)
C;Species: Pachnoda marginata
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S21663
R;Gaede, G.; Lopata, A.; Kellner, R.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 373, 133-142, 1992
A;Title: Primary structures of neuropeptides isolated from the corpora cardiaca of va
ectrometry.
A;Reference number: S21663; MUID:92265187
A;Accession: S21663
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <GAE>

Query Match 50.0%; Score 21; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      3 EKKYSP 8
          |  |||
Db      1 ELNYSP 6
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RESULT 2
S15422
adipokinetic hormone - cockchafer
C;Species: Melolontha melolontha (cockchafer)
C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: S15422
R;Gaede, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red
A;Reference number: S15422; MUID:91248100
A;Accession: S15422
A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 42.9%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      6 YSP 8
          |||
Db      4 YSP 6
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```
RESULT   3
A58641
adipokinetic hormone - dor beetle
C;Species: Geotrupes stercorosus (dor beetle)
C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: A58641
R;Gaede, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-pi
A;Reference number: S15422; MUID:91248100
A;Accession: A58641
A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

  Query Match             42.9%;  Score 18;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 YSP 8
           |||
Db       4 YSP 6


RESULT   4
A05169
neuropeptide M-I - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993
C;Accession: A05169
R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mas
A;Reference number: A90118; MUID:85046530
A;Accession: A05169
A;Molecule type: protein
A;Residues: 1-8 <WIT>
C;Keywords: neuropeptide

  Query Match             40.5%;  Score 17;  DB 2;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+05;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 EKKYSP 8
           |  :||
Db       1 EVNFSP 6


RESULT   5
S20162
leghemoglobin III - Sesbania rostrata (fragment)
C;Species: Sesbania rostrata
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 04-Mar-2000
C;Accession: S20162
R;Metz, B.A.; Welters, P.; Hoffmann, H.J.; Jensen, E.O.; Schell, J.; de Bruijn, F.J.
Mol. Gen. Genet. 214, 181-191, 1988
A;Title: Primary structure and promoter analysis of leghemoglobin genes of the stem-nodu
A;Reference number: S08322; MUID:89181515
A;Accession: S20162
A;Molecule type: DNA
A;Residues: 1-8 <MET>
A;Cross-references: EMBL:X13504; NID:g21383; PIDN:CAA31858.1; PID:g579482
C;Genetics:
A;Gene: glb3
C;Superfamily: globin; globin homology
C;Keywords: heme; oxygen carrier

  Query Match             38.1%;  Score 16;  DB 2;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 2.2e+05;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TEKK 5
           |||:
Db       4 TEKQ 7


RESULT   6
A14683
aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fr
N;Alternate names: aspartate aminotransferase, mitochondrial
C;Species: Gallus gallus (chicken)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C;Accession: A14683
R;Wilson, K.J.; Hunziker, P.; Hughes, G.J.
FEBS Lett. 108, 98-102, 1979
A;Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.
A;Reference number: A14683; MUID:80092116
A;Accession: A14683
A;Molecule type: protein
A;Residues: 1-8 <WIL>
C;Keywords: aminotransferase; mitochondrion

  Query Match             38.1%;  Score 16;  DB 2;  Length 8;
  Best Local Similarity   28.6%;  Pred. No. 2.2e+05;
  Matches    2;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 TEKKYSP 8
           :|  : |
Db       1 SENNFQP 7


RESULT   7
S45651
probable Na+-transporting ATP synthase (EC 3.6.1.-) - Acetobacterium woodii (fragment
C;Species: Acetobacterium woodii
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
C;Accession: S45651
R;Reidlinger, J.; Mueller, V.
Eur. J. Biochem. 223, 275-283, 1994
A;Title: Purification of ATP synthase from Acetobacterium woodii and identification a
A;Reference number: S45648; MUID:94307271
A;Accession: S45651
A;Molecule type: protein
A;Residues: 1-8 <REI>
A;Experimental source: DSM 1030
C;Keywords: hydrolase

  Query Match             38.1%;  Score 16;  DB 2;  Length 8;
  Best Local Similarity   42.9%;  Pred. No. 2.2e+05;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 LTEKKYS 7
           |   ||:
Db       2 LVASKYA 8


RESULT   8
A61348
red pigment-concentrating hormone - northern shrimp
N;Alternate names: blanching hormone
C;Species: Pandalus borealis (northern shrimp)
C;Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C;Accession: A61348; S07139
R;Fernlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A;Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
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A;Reference number: A61348; MUID:72228738
A;Accession: A61348
A;Molecule type: protein
A;Residues: 1-8 <FER1>
R;Fernlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A;Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus bore
A;Reference number: S07139; MUID:75054965
A;Accession: S07139
A;Molecule type: protein
A;Residues: 'E',2-8 <FER2>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pi
zed pigment-containing cells.
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutami
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 33.3%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YSP 8
:||
Db 4 FSP 6

RESULT 9
S08995
hypertrehalosemic hormone I - oriental cockroach
N;Alternate names: Pea-CAH-I
C;Species: Blatta orientalis (oriental cockroach)
C;Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C;Accession: S08995
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpor
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A;Reference number: S08995; MUID:90253659
A;Accession: S08995
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 33.3%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YSP 8
:||
Db 4 FSP 6

RESULT 10
A49823
adipokinetic hormone I - American cockroach
N;Alternate names: periplanetin CC-1
C;Species: Periplaneta americana (American cockroach)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Accession: A49823
R;Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp
A;Reference number: A49823; MUID:84298179
A;Accession: A49823
A;Molecule type: protein
A;Residues: 1-8 <SCA>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 33.3%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YSP 8
:||
Db 4 FSP 6

RESULT 11
A44960
neuropeptide Led-CC-I - Colorado potato beetle
C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A44960
R;Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle a
A;Reference number: A44960; MUID:90160053
A;Accession: A44960
A;Molecule type: protein
A;Residues: 1-8 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutam
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimenta

Query Match 33.3%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YSP 8
:||
Db 4 FSP 6

RESULT 12
A43976
hypertrehalosemic hormone - yellow mealworm
C;Species: Tenebrio molitor (yellow mealworm)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 07-May-1999
C;Accession: A43976
R;Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid
A;Reference number: A43976; MUID:90341081
A;Accession: A43976
A;Molecule type: protein
A;Residues: 1-8 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 33.3%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YSP 8
:||
Db 4 FSP 6

RESULT 13

B43976
hypertrehalosemic hormone - beetle (Zophobas rugipes)
C;Species: Zophobas rugipes
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 07-May-1999
C;Accession: B43976
R;Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid be
A;Reference number: A43976; MUID:90341081
A;Accession: B43976
A;Molecule type: protein
A;Residues: 1-8 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 33.3%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YSP 8
:||
Db 4 FSP 6

RESULT 14
S11545
adipokinetic hormone - nestling-sucking blowfly
C;Species: Protophormia terraenovae (nestling-sucking blowfly)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 31-Oct-1997
C;Accession: S11545
R;Gaede, G.; Wilps, H.; Kellner, R.
Biochem. J. 269, 309-313, 1990
A;Title: Isolation and structure of a novel charged member of the red-pigment-concentrat
erraenovae (Diptera).
A;Reference number: S11545; MUID:90351345
A;Accession: S11545
A;Molecule type: protein
A;Residues: 1-8 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 33.3%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YSP 8
:||
Db 4 FSP 6

RESULT 15
D47393
neuropeptide callatostatin 4 - bluebottle fly (Calliphora vomitoria)
C;Species: Calliphora vomitoria
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
C;Accession: D47393
R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
A;Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequen
A;Reference number: A47393; MUID:93211980
A;Accession: D47393
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <DUV>
A;Experimental source: thoracic ganglia
A;Note: sequence extracted from NCBI backbone (NCBIP:128479)

Query Match 33.3%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EKKYS 7
:: ||
Db 1 DRPYS 5

Search completed: December 13, 2001, 11:56:34
Job time: 57 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 11:56:37 ; Search time 12.48 Seconds
(without alignments)
23.503 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 64

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	45.2	8	1	UH09_RAT	P56575 rattus norv
2	18	42.9	8	1	AKH_MELML	P25423 melolontha
3	14	33.3	8	1	ALL4_CALVO	P41840 calliphora
4	14	33.3	8	1	HTF1_PERAM	P04548 periplaneta
5	14	33.3	8	1	HTF_TENMO	P25419 tenebrio mo
6	14	33.3	8	1	RPCH_PANBO	P08939 pandalus bo
7	13	31.0	8	1	LMT2_LOCMI	P22396 locusta mig
8	12	28.6	8	1	AL17_CARMA	P81820 carcinus ma
9	12	28.6	8	1	ALL3_CYDPO	P82154 cydia pomon
10	12	28.6	8	1	ALL4_CYDPO	P82155 cydia pomon
11	12	28.6	8	1	LPK_LEUMA	P13049 leucophaea
12	11	26.2	8	1	AKH_LIBAU	P25418 libellula a
13	11	26.2	8	1	AKH_TABAT	P14595 tabanus atr
14	11	26.2	8	1	AL15_CARMA	P81818 carcinus ma
15	11	26.2	8	1	AL16_CARMA	P81819 carcinus ma
16	11	26.2	8	1	AL18_CARMA	P81821 carcinus ma
17	11	26.2	8	1	ALL1_CYDPO	P82152 cydia pomon
18	11	26.2	8	1	ALL7_CARMA	P81809 carcinus ma
19	11	26.2	8	1	HTF2_PERAM	P04549 periplaneta
20	11	26.2	8	1	LCK8_LEUMA	P19990 leucophaea
21	11	26.2	8	1	PPK2_PERAM	P82692 periplaneta
22	10	23.8	8	1	FAR4_HOMAM	P41487 homarus ame
23	10	23.8	8	1	NPB_BOVIN	P15507 bos taurus
24	9	21.4	8	1	ACI_THUAL	P18691 thunnus alb
25	9	21.4	8	1	ANG2_BOTJA	Q10582 bothrops ja
26	9	21.4	8	1	B44K_PORGI	P81886 porphyromon
27	9	21.4	8	1	UPAA_HUMAN	P30096 homo sapien
28	8	19.0	8	1	AL12_CARMA	P81815 carcinus ma
29	8	19.0	8	1	ALL6_CYDPO	P82157 cydia pomon
30	8	19.0	8	1	ALL8_CARMA	P81811 carcinus ma
31	8	19.0	8	1	ALL9_CARMA	P81812 carcinus ma
32	8	19.0	8	1	CLP_THICU	P80488 thiobacillu
33	8	19.0	8	1	FAR3_HOMAM	P41486 homarus ame
34	8	19.0	8	1	RS7_MYCIT	P33564 mycobacteri
35	7	16.7	8	1	ACT_CARMA	P80709 carcinus ma
36	7	16.7	8	1	AKHG_GRYBI	P14086 gryllus bim
37	7	16.7	8	1	ALL5_CALVO	P41841 calliphora
38	7	16.7	8	1	ALL5_CYDPO	P82156 cydia pomon
39	7	16.7	8	1	CAD1_ENTFA	P13268 enterococcu
40	7	16.7	8	1	CCKN_MACEU	P30369 macropus eu
41	7	16.7	8	1	FAR1_PANRE	P41872 panagrellus
42	7	16.7	8	1	FAR7_ASCSU	P43171 ascaris suu
43	7	16.7	8	1	FUSS_FUSSO	P81010 fusarium so
44	7	16.7	8	1	GLUR_HUMAN	P02729 homo sapien
45	7	16.7	8	1	LCK1_LEUMA	P21140 leucophaea

ALIGNMENTS

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RESULT   1
UH09_RAT
ID   UH09_RAT       STANDARD;      PRT;     8 AA.
AC   P56575;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   UNKNOWN PROTEIN FROM 2D-PAGE OF HEART TISSUE (SPOT P9) (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=WISTAR; TISSUE=Heart;
RA   Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA   Jungblut P.R.;
RL   Submitted (SEP-1998) to the SWISS-PROT data bank.
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 8.9, ITS MW IS: 42 KDA.
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  1029 MW;  9E0775A6C4140B06 CRC64;


  Query Match             45.2%;  Score 19;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+05;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 EKKYSP 8
           |:: ||
Db       2 ERRQSP 7


RESULT   2
AKH_MELML
ID   AKH_MELML      STANDARD;      PRT;     8 AA.
AC   P25423;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   ADIPOKINETIC HORMONE (AKH).
OS   Melolontha melolontha (Cockchafer),
OS   Geotrupes stercorosus (Dor beetle), and
OS   Pachnoda marginata (Flower beetle).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC   Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
OX   NCBI_TaxID=7061, 7087, 7058;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
RX   MEDLINE=91248100; PubMed=2039445;
RA   Gaede G.;
RT   "A unique charged tyrosine-containing member of the adipokinetic
RT   hormone/red-pigment-concentrating hormone peptide family isolated and
RT   sequenced from two beetle species.";
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RL   Biochem. J. 275:671-677(1991).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=P.marginata; TISSUE=Corpora cardiaca;
RX   MEDLINE=92265187; PubMed=1586453;
RA   Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
RT   "Primary structures of neuropeptides isolated from the corpora
RT   cardiaca of various cetonid beetle species determined by
RT   pulsed-liquid phase sequencing and tandem fast atom bombardment mass
RT   spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 373:133-142(1992).
CC   -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC       CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC       DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC       MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; S15422; S15422.
DR   PIR; S21663; S21663.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Flight.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  1022 MW;  867AB775AB544736 CRC64;


  Query Match             42.9%;  Score 18;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 YSP 8
           |||
Db       4 YSP 6


RESULT   3
ALL4_CALVO
ID   ALL4_CALVO     STANDARD;      PRT;     8 AA.
AC   P41840;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CALLATOSTATIN 4 (LEU-CALLATOSTATIN 4).
OS   Calliphora vomitoria (Blue blowfly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Oestroidea; Calliphoridae; Calliphora.
OX   NCBI_TaxID=27454;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Thoracic ganglion;
RX   MEDLINE=93211980; PubMed=8460157;
RA   Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA   Thorpe A.;
RT   "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria
RT   with sequence homology to cockroach allatostatins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN   [2]
RP   CHARACTERIZATION.
RX   MEDLINE=94291167; PubMed=8020069;
RA   Duve H., Thorpe A.;
RT   "Distribution and functional significance of Leu-callatostatins in
RT   the blowfly Calliphora vomitoria.";
RL   Cell Tissue Res. 276:367-379(1994).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
CC       A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
CC       INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
CC       BEHAVE AS POTENT INHIBITORS OF PERISTALIC MOVEMENTS, MAY ALSO
CC       FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC   -!- TISSUE SPECIFICITY: BRAIN, SUBOESOPHAGEAL GANGLION, RETROCEREBRAL
CC       COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY
CC       SYSTEM AND INTESTINE.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR   PIR; D47393; D47393.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8      8       AMIDATION.
FT   UNSURE        1      1       OR N.
SQ   SEQUENCE   8 AA;  954 MW;  D32879D5AB47740A CRC64;


  Query Match             33.3%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 EKKYS 7
           :: ||
Db       1 DRPYS 5


RESULT   4
HTF1_PERAM
ID   HTF1_PERAM     STANDARD;      PRT;     8 AA.
AC   P04548;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   HYPERTREHALOSAEMIC FACTOR I (NEUROPEPTIDE M-I) (PERIPLANETIN CC-I)
DE   (PEA-CAH-I) (LED-CC-I) (HYPERTREHALOSAEMIC NEUROPEPTIDE I).
OS   Periplaneta americana (American cockroach),
OS   Leptinotarsa decemlineata (Colorado potato beetle), and
OS   Blatta orientalis (Oriental cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blattoidea; Blattidae; Periplaneta.
OX   NCBI_TaxID=6978, 7539, 6976;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=P.americana;
RX   MEDLINE=85046530; PubMed=6548628;
RA   Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA   Rinehart K.L. Jr.;
RT   "Structures of two cockroach neuropeptides assigned by fast atom
RT   bombardment mass spectrometry.";
RL   Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=P.americana;
RX   MEDLINE=84298179; PubMed=6591205;
RA   Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA   Miller C.A., Schooley D.A.;
RT   "Isolation and primary structure of two peptides with
RT   cardioacceleratory and hyperglycemic activity from the corpora
RT   cardiaca of Periplaneta americana.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX   MEDLINE=90160053; PubMed=2576128;
RA   Gaede G., Kellner R.;
RT   "The metabolic neuropeptides of the corpus cardiacum from the potato
RT   beetle and the American cockroach are identical.";
RL   Peptides 10:1287-1289(1989).
RN   [4]
RP   SEQUENCE.
RC   SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX   MEDLINE=90253659; PubMed=2340112;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT   the corpora cardiaca of the cockroaches Leucophaea maderae,
RT   Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT   and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT   atom bombardment mass spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC   -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC       ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC       THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
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CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; A05169; A05169.
DR   PIR; S08995; S08995.
DR   PIR; A49823; A49823.
DR   PIR; A44960; A44960.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  991 MW;  86745775B9C452D6 CRC64;


  Query Match             33.3%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 YSP 8
          :||
Db      4 FSP 6


RESULT   5
HTF_TENMO
ID   HTF_TENMO      STANDARD;      PRT;     8 AA.
AC   P25419;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   HYPERTREHALOSAEMIC FACTOR (HOTH) (HYPERTREHALOSEMIC NEUROPEPTIDE).
OS   Tenebrio molitor (Yellow mealworm), and Zophobas rugipes.
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC   Cucujiformia; Tenebrionidae; Tenebrio.
OX   NCBI_TaxID=7067, 7075;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=90341081; PubMed=2381871;
RA   Gaede G., Rosinski G.;
RT   "The primary structure of the hypertrehalosemic neuropeptide from
RT   tenebrionid beetles: a novel member of the AKH/RPCH family.";
RL   Peptides 11:455-459(1990).
CC   -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC       ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC       THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; A43976; A43976.
DR   PIR; B43976; B43976.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  1005 MW;  86745775B9C44736 CRC64;


  Query Match             33.3%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 YSP 8
          :||
Db      4 FSP 6


RESULT   6
RPCH_PANBO
ID   RPCH_PANBO     STANDARD;      PRT;     8 AA.
AC   P08939;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   RED PIGMENT CONCENTRATING HORMONE (RPCH).
OS   Pandalus borealis (Northern red shrimp).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidea;
OC   Pandalidae; Pandalus.
OX   NCBI_TaxID=6703;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75054965; PubMed=4433569;
RA   Fernlund P.;
RT   "Structure of the red-pigment-concentrating hormone of the shrimp,
RT   Pandalus borealis.";
RL   Biochim. Biophys. Acta 371:304-311(1974).
CC   -!- FUNCTION: THIS HORMONE ADAPTS THE ANIMAL TO LIGHT BACKGROUNDS BY
CC       STIMULATING CONCENTRATION OF THE PIGMENT OF ITS RED BODY-
CC       CHROMATOPHORES.
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; S07139; S07139.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Pigment; Hormone; Amidation.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  948 MW;  86786775B9C44736 CRC64;


  Query Match             33.3%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 YSP 8
          :||
Db      4 FSP 6


RESULT   7
LMT2_LOCMI
ID   LMT2_LOCMI     STANDARD;      PRT;     8 AA.
AC   P22396;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   01-AUG-1991 (Rel. 19, Last annotation update)
DE   LOCUSTAMYOTROPIN 2 (LOM-MT-2).
OS   Locusta migratoria (Migratory locust).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC   Acridomorpha; Acridoidea; Acrididae; Locusta.
OX   NCBI_TaxID=7004;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RA   Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT   "Isolation, identification and synthesis of locustamyotropin II, an
RT   additional neuropeptide of Locusta migratoria. Member of the
RT   cephalomyotropic peptide family.";
RL   Insect Biochem. 20:479-484(1990).
CC   -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC       (MYOTROPIC ACTIVITY).
CC   -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR   InterPro; IPR001484; Pyrokinin.
DR   PROSITE; PS00539; PYROKININ; 1.
KW   Neuropeptide; Amidation; Pyrokinin.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  934 MW;  26341771A9CAA87B CRC64;


  Query Match             31.0%;  Score 13;  DB 1;  Length 8;
  Best Local Similarity   33.3%;  Pred. No. 1e+05;
  Matches    2;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      3 EKKYSP 8
            |  ::|
Db      1 EGDFTP 6
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RESULT   8
AL17_CARMA
ID   AL17_CARMA     STANDARD;      PRT;     8 AA.
AC   P81820;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 17.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       8       8       AMIDATION (POTENTIAL).
SQ   SEQUENCE   8 AA;  858 MW;  C82879D5AB46D865 CRC64;


  Query Match             28.6%;  Score 12;  DB 1;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 KYS 7
           :||
Db       3 QYS 5


RESULT   9
ALL3_CYDPO
ID   ALL3_CYDPO     STANDARD;      PRT;     8 AA.
AC   P82154;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CYDIASTATIN 3.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  926 MW;  C82879D5AB477415 CRC64;


  Query Match             28.6%;  Score 12;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 KKYS 7
           : ||
Db       2 RPYS 5


RESULT  10
ALL4_CYDPO
ID   ALL4_CYDPO     STANDARD;      PRT;     8 AA.
AC   P82155;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CYDIASTATIN 4.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  910 MW;  922879D5AB47740D CRC64;


  Query Match             28.6%;  Score 12;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 KKYS 7
           : ||
Db       2 RPYS 5


RESULT  11
LPK_LEUMA
ID   LPK_LEUMA      STANDARD;      PRT;     8 AA.
AC   P13049;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   LEUKOPYROKININ (LPK) (LEM-PK).
OS   Leucophaea maderae (Madeira cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blaberoidea; Blaberidae; Leucophaea.
OX   NCBI_TaxID=6988;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86269041; PubMed=3015140;
RA   Nachman R.J., Holman G.M., Cook B.J.;
RT   "Active fragments and analogs of the insect neuropeptide
RT   leucopyrokinin: structure-function studies.";
RL   Biochem. Biophys. Res. Commun. 137:936-942(1986).
RN   [2]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Head;
RX   MEDLINE=87052651; PubMed=2877794;
RA   Holman G.M., Cook B.J., Nachman R.J.;
RT   "Primary structure and synthesis of a blocked myotropic
RT   neuropeptide isolated from the cockroach, Leucophaea maderae.";
RL   Comp. Biochem. Physiol. 85C:219-224(1986).
CC   -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC       (MYOTROPIC ACTIVITY).
CC   -!- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS
CC       SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE
CC       PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPK MOST
CC       CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE
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CC       PENTAPEPTIDE FRAGMENT FTPRL.
CC   -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR   PIR; A23967; A23967.
DR   InterPro; IPR001484; Pyrokinin.
DR   PROSITE; PS00539; PYROKININ; 1.
KW   Neuropeptide; Amidation; Pyrokinin.
FT   MOD_RES       1       1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  949 MW;  92341771A9D5A1B6 CRC64;


  Query Match             28.6%;  Score 12;  DB 1;  Length 8;
  Best Local Similarity   16.7%;  Pred. No. 1e+05;
  Matches    1;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      3 EKKYSP 8
          :  ::|
Db      1 QTSFTP 6


RESULT  12
AKH_LIBAU
ID   AKH_LIBAU      STANDARD;      PRT;     8 AA.
AC   P25418;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   ADIPOKINETIC HORMONE (AKH).
OS   Libellula auripennis (Skimmer dragonfly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX   NCBI_TaxID=6966;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=90359055; PubMed=2390213;
RA   Gaede G.;
RT   "The putative ancestral peptide of the adipokinetic/red-pigment-
RT   concentrating hormone family isolated and sequenced from a
RT   dragonfly.";
RL   Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC   -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC       CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC       DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC       MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; S10596; S10596.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Flight.
FT   MOD_RES       1       1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  978 MW;  8665A771A9C452D6 CRC64;


  Query Match             26.2%;  Score 11;  DB 1;  Length 8;
  Best Local Similarity   33.3%;  Pred. No. 1e+05;
  Matches    1;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 YSP 8
          ::|
Db      4 FTP 6


RESULT  13
AKH_TABAT
ID   AKH_TABAT      STANDARD;      PRT;     8 AA.
AC   P14595;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   ADIPOKINETIC HORMONE (AKH) (DIPTERAN CORPORA CARDIACA FACTOR I)
DE   (DCC I).
OS   Tabanus atratus (Horse fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
OC   Tabanidae; Tabanus.
OX   NCBI_TaxID=7207;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=90046758; PubMed=2813385;
RA   Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA   Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT   "Primary structure of two neuropeptide hormones with adipokinetic and
RT   hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT   flies (Diptera).";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC   -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC       CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC       DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC       MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; A33995; A33995.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Flight.
FT   MOD_RES       1       1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  949 MW;  86786771A9D1A736 CRC64;


  Query Match             26.2%;  Score 11;  DB 1;  Length 8;
  Best Local Similarity   33.3%;  Pred. No. 1e+05;
  Matches    1;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 YSP 8
          ::|
Db      4 FTP 6


RESULT  14
AL15_CARMA
ID   AL15_CARMA     STANDARD;      PRT;     8 AA.
AC   P81818;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 15.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  811 MW;  922879D5AB47687D CRC64;


  Query Match             26.2%;  Score 11;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 YS 7
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```
Db      4 YS 5


RESULT  15
AL16_CARMA
ID   AL16_CARMA     STANDARD;      PRT;     8 AA.
AC   P81819;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 16.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  813 MW;  7C286B45AB476878 CRC64;


  Query Match             26.2%;  Score 11;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 YS 7
          ||
Db      4 YS 5


Search completed: December 13, 2001, 12:01:34
Job time: 297 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 11:55:37 ; Search time 36.87 Seconds
(without alignments)
16.072 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 15187

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	57.1	8	16	AAW21215	Farnesyl synthetas
2	24	57.1	8	16	AAW21216	Farnesyl synthetas
3	21	50.0	8	14	AAR36175	Hepatitis C virus
4	21	50.0	8	20	AAY08147	Clotting factor VI
5	21	50.0	8	20	AAY08148	Clotting factor VI
6	21	50.0	8	20	AAY08149	Clotting factor VI
7	21	50.0	8	20	AAY08150	Clotting factor VI
8	20	47.6	8	16	AAR79692	pp60(c-src) kinase
9	20	47.6	8	18	AAW39531	HIV-1 pol peptide
10	20	47.6	8	20	AAY19720	SEQ ID NO 438 from
11	20	47.6	8	21	AAY57993	Mouse polyoma midd
12	19	45.2	8	15	AAR72419	Recombinant timoth
13	19	45.2	8	16	AAR79693	pp60(c-src) kinase
14	19	45.2	8	17	AAW05444	SH2-binding peptid
15	19	45.2	8	20	AAY47205	Immunogenic peptid
16	19	45.2	8	20	AAY24894	Peptide Vif 88-95.
17	19	45.2	8	20	AAY10292	T cell epitope/MHC
18	19	45.2	8	20	AAW94115	VIF-derived HIV pr
19	19	45.2	8	21	AAB33495	Mouse immunoglobul
20	19	45.2	8	21	AAY57994	Hamster polyoma mi
21	18	42.9	8	13	AAR27014	Peptide used in an
22	18	42.9	8	13	AAR27016	Peptide used in an
23	18	42.9	8	14	AAR36250	Hepatitis C virus
24	18	42.9	8	14	AAR36251	Hepatitis C virus
25	18	42.9	8	14	AAR36252	Hepatitis C virus
26	18	42.9	8	14	AAR36253	Hepatitis C virus
27	18	42.9	8	14	AAR42770	Consensus peptide,
28	18	42.9	8	15	AAR55737	Protein-kinase inh
29	18	42.9	8	15	AAR55738	Phosphorylase-kina
30	18	42.9	8	16	AAR79474	HIV gag p17 nuclea
31	18	42.9	8	16	AAR70582	HIV(B35)-1, human
32	18	42.9	8	16	AAR73574	Human TSH receptor
33	18	42.9	8	16	AAR73573	Human TSH receptor
34	18	42.9	8	17	AAR98080	Peptide for use in
35	18	42.9	8	17	AAR98058	Peptide for use in
36	18	42.9	8	17	AAR98060	Peptide for use in
37	18	42.9	8	17	AAR88101	Bovine p32 11-cis-
38	18	42.9	8	17	AAR88489	PECAM-1 gene exon
39	18	42.9	8	18	AAW18339	Bovine p32 11-cis-
40	18	42.9	8	19	AAW64278	mMCP-7 peptide sub
41	18	42.9	8	19	AAW79168	Conserved sequence
42	18	42.9	8	19	AAW53299	CS4-CFA/I family s
43	18	42.9	8	19	AAW53300	CS4-CFA/I family s
44	18	42.9	8	20	AAY39614	CTLA-4 VLD CDR1 re
45	18	42.9	8	22	AAB46258	HPV type 16 cytoto

ALIGNMENTS

RESULT 1
AAW21215
ID AAW21215 standard; peptide; 8 AA.
XX
AC AAW21215;
XX
DT 29-JUL-1997 (first entry)
XX
DE Farnesyl synthetase derived signal oligopeptide #15.
XX
KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.
XX
OS Homo sapiens.
XX
PN WO9519568-A1.
XX
PD 20-JUL-1995.
XX
PF 12-JAN-1995; 95WO-US00575.
XX
PR 14-JAN-1994; 94US-0182248.
XX
PA (RATH/) RATH M.
XX

PI Rath M;
XX
DR WPI; 1995-263953/34.
XX
PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication
PT between protein(s)
XX
PS Claim 5; Page 25; 88pp; English.
XX
CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC peptides. These signal oligopeptides are localised on the surface
CC of the protein and are represented by the hydrophilicity maxima of
CC the protein. These peptides are enriched in charged amino acids
CC arranged with neutral spacer amino acids. The specific signal
CC character of these oligopeptides is determined by a characteristic
CC combination of conformation and charge within the signal sequence.
CC These oligopeptides may be used as vaccines in the treatment of
CC human disease, as competitive inhibitors to prevent or reduce the
CC metabolic action or interaction of a selected protein by blocking
CC its specific signal sequences, or as therapeutic agents to function
CC as feedback regulators to reduce synthesis rate of a selected protein.
CC These peptides may be modified by omitting one or more amino acids at
CC the N- and/or C-terminal, by substituting one or more amino acids
CC without consideration of charge and polarity, by substituting one or
CC more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these.
XX
SQ Sequence 8 AA;

Query Match 57.1%; Score 24; DB 16; Length 8;
Best Local Similarity 80.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TEKKY 6
||| :|
Db 3 tekry 7

RESULT 2
AAW21216
ID AAW21216 standard; peptide; 8 AA.
XX
AC AAW21216;
XX
DT 29-JUL-1997 (first entry)
XX
DE Farnesyl synthetase derived signal oligopeptide #16.
XX
KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.
XX
OS Homo sapiens.
XX
PN WO9519568-A1.
XX
PD 20-JUL-1995.
XX
PF 12-JAN-1995; 95WO-US00575.
XX
PR 14-JAN-1994; 94US-0182248.
XX
PA (RATH/) RATH M.

XX
PI Rath M;
XX
DR WPI; 1995-263953/34.
XX
PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication
PT between protein(s)
XX
PS Claim 5; Page 25; 88pp; English.
XX
CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC peptides. These signal oligopeptides are localised on the surface
CC of the protein and are represented by the hydrophilicity maxima of
CC the protein. These peptides are enriched in charged amino acids
CC arranged with neutral spacer amino acids. The specific signal
CC character of these oligopeptides is determined by a characteristic
CC combination of conformation and charge within the signal sequence.
CC These oligopeptides may be used as vaccines in the treatment of
CC human disease, as competitive inhibitors to prevent or reduce the
CC metabolic action or interaction of a selected protein by blocking
CC its specific signal sequences, or as therapeutic agents to function
CC as feedback regulators to reduce synthesis rate of a selected protein.
CC These peptides may be modified by omitting one or more amino acids at
CC the N- and/or C-terminal, by substituting one or more amino acids
CC without consideration of charge and polarity, by substituting one or
CC more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these.
XX
SQ Sequence 8 AA;

Query Match 57.1%; Score 24; DB 16; Length 8;
Best Local Similarity 80.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TEKKY 6
||| :|
Db 3 tekry 7

RESULT 3
AAR36175
ID AAR36175 standard; peptide; 8 AA.
XX
AC AAR36175;
XX
DT 24-MAY-1993 (first entry)
XX
DE Hepatitis C virus (HCV) epitope EpEE.
XX
KW Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;
KW immobilised reagent; immunoassay; diagnosis; detection; treatment;
KW infection.
XX
OS Hepatitis C virus type 1.
XX
PN WO9300365-A.
XX
PD 07-JAN-1993.
XX
PF 24-JUN-1992; 92WO-US05388.
XX
PR 24-JUN-1991; 91US-0722489.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chien DY, Rutter W;
XX
DR WPI; 1993-036334/04.
XX
PT Polypeptide(s) comprising truncated hepatitis C virus sequences -
PT for detection, prevention and treatment of hepatitis C infection

```
XX
PS   Example A; Page 39; 80pp; English.
XX
CC   This octamer was found to be immunoreactive with anti-HCV anti-sera.
CC   In the epitope mapping experiment three different samples of anti-sera
CC   were reacted with the peptide octamer, and then incubated with
CC   HRP-labelled goat anti-human Ig antisera, to enable detection of
CC   binding. This epitope starts from amino acid 2676 of the HCV
CC   polyprotein.
CC   This was found to be a particulary strong epitope.
XX
SQ   Sequence   8 AA;


  Query Match             50.0%;  Score 21;  DB 14;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 4.3e+05;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 LTEKKY 6
           |||: |
Db       1 lterly 6


RESULT   4
AAY08147
ID   AAY08147 standard; peptide; 8 AA.
XX
AC   AAY08147;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Clotting factor VIII binding peptide 29.
XX
KW   Coagulation factor VIII; clotting factor VIII; diagnosis; treatment;
KW   purification; disorder; blood coagulation.
XX
OS   Synthetic.
XX
PN   WO9914232-A1.
XX
PD   25-MAR-1999.
XX
PF   12-SEP-1998;   98WO-EP05822.
XX
PR   13-SEP-1997;   97DE-1040310.
XX
PA   (OCTA-) OCTAPHARMA AG.
XX
PI   Jungbauer A;
XX
DR   WPI; 1999-312410/26.
XX
PT   Peptides with affinity for blood clotting factor 8
XX
PS   Claim 4; Page 26; 51pp; German.
XX
CC   This invention describes novel peptides (AAY08119-Y08212) with affinity
CC   for coagulation factor VIII which can be used for for labeling,
CC   identification (diagnostic) and purification of factor VIII. Some are
CC   specific for one of natural and recombinant factor VIII, others are
CC   reactive with both forms. Factor VIII is used to treat disorders of
CC   blood coagulation. Using relatively small peptides, rather than large
CC   antibody molecules generally used, simplifies purification of factor
CC   VIII. The peptides are of formula R1-X-R2 where R1 = amino or a
CC   peptide; R2 = carboxy or a peptide and X = a peptide of at least 3,
CC   preferably 7-12, amino acid residues.
XX
SQ   Sequence   8 AA;


  Query Match             50.0%;  Score 21;  DB 20;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 4.3e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KKYSP 8
           |:|:|
Db       4 keyap 8


RESULT   5
AAY08148
ID   AAY08148 standard; peptide; 8 AA.
XX
AC   AAY08148;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Clotting factor VIII binding peptide 30.
XX
KW   Coagulation factor VIII; clotting factor VIII; diagnosis; treatment;
KW   purification; disorder; blood coagulation.
XX
OS   Synthetic.
XX
PN   WO9914232-A1.
XX
PD   25-MAR-1999.
XX
PF   12-SEP-1998;   98WO-EP05822.
XX
PR   13-SEP-1997;   97DE-1040310.
XX
PA   (OCTA-) OCTAPHARMA AG.
XX
PI   Jungbauer A;
XX
DR   WPI; 1999-312410/26.
XX
PT   Peptides with affinity for blood clotting factor 8
XX
PS   Claim 4; Page 26; 51pp; German.
XX
CC   This invention describes novel peptides (AAY08119-Y08212) with affinity
CC   for coagulation factor VIII which can be used for for labeling,
CC   identification (diagnostic) and purification of factor VIII. Some are
CC   specific for one of natural and recombinant factor VIII, others are
CC   reactive with both forms. Factor VIII is used to treat disorders of
CC   blood coagulation. Using relatively small peptides, rather than large
CC   antibody molecules generally used, simplifies purification of factor
CC   VIII. The peptides are of formula R1-X-R2 where R1 = amino or a
CC   peptide; R2 = carboxy or a peptide and X = a peptide of at least 3,
CC   preferably 7-12, amino acid residues.
XX
SQ   Sequence   8 AA;


  Query Match             50.0%;  Score 21;  DB 20;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 4.3e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 KKYSP 8
           |:|:|
Db       3 keyap 7


RESULT   6
AAY08149
ID   AAY08149 standard; peptide; 8 AA.
XX
AC   AAY08149;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Clotting factor VIII binding peptide 31.
XX
KW   Coagulation factor VIII; clotting factor VIII; diagnosis; treatment;
```

KW purification; disorder; blood coagulation.
XX
OS Synthetic.
XX
PN WO9914232-A1.
XX
PD 25-MAR-1999.
XX
PF 12-SEP-1998; 98WO-EP05822.
XX
PR 13-SEP-1997; 97DE-1040310.
XX
PA (OCTA-) OCTAPHARMA AG.
XX
PI Jungbauer A;
XX
DR WPI; 1999-312410/26.
XX
PT Peptides with affinity for blood clotting factor 8
XX
PS Claim 4; Page 27; 51pp; German.
XX
CC This invention describes novel peptides (AAY08119-Y08212) with affinity
CC for coagulation factor VIII which can be used for for labeling,
CC identification (diagnostic) and purification of factor VIII. Some are
CC specific for one of natural and recombinant factor VIII, others are
CC reactive with both forms. Factor VIII is used to treat disorders of
CC blood coagulation. Using relatively small peptides, rather than large
CC antibody molecules generally used, simplifies purification of factor
CC VIII. The peptides are of formula R1-X-R2 where R1 = amino or a
CC peptide; R2 = carboxy or a peptide and X = a peptide of at least 3,
CC preferably 7-12, amino acid residues.
XX
SQ Sequence 8 AA;

Query Match 50.0%; Score 21; DB 20; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKYSP 8
|:|:|
Db 2 keyap 6

RESULT 7
AAY08150
ID AAY08150 standard; peptide; 8 AA.
XX
AC AAY08150;
XX
DT 09-JUL-1999 (first entry)
XX
DE Clotting factor VIII binding peptide 32.
XX
KW Coagulation factor VIII; clotting factor VIII; diagnosis; treatment;
KW purification; disorder; blood coagulation.
XX
OS Synthetic.
XX
PN WO9914232-A1.
XX
PD 25-MAR-1999.
XX
PF 12-SEP-1998; 98WO-EP05822.
XX
PR 13-SEP-1997; 97DE-1040310.
XX
PA (OCTA-) OCTAPHARMA AG.
XX
PI Jungbauer A;
XX
DR WPI; 1999-312410/26.
XX
PT Peptides with affinity for blood clotting factor 8
XX
PS Claim 4; Page 27; 51pp; German.
XX
CC This invention describes novel peptides (AAY08119-Y08212) with affinity
CC for coagulation factor VIII which can be used for for labeling,
CC identification (diagnostic) and purification of factor VIII. Some are
CC specific for one of natural and recombinant factor VIII, others are
CC reactive with both forms. Factor VIII is used to treat disorders of
CC blood coagulation. Using relatively small peptides, rather than large
CC antibody molecules generally used, simplifies purification of factor
CC VIII. The peptides are of formula R1-X-R2 where R1 = amino or a
CC peptide; R2 = carboxy or a peptide and X = a peptide of at least 3,
CC preferably 7-12, amino acid residues.
XX
SQ Sequence 8 AA;

Query Match 50.0%; Score 21; DB 20; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KKYSP 8
|:|:|
Db 1 keyap 5

RESULT 8
AAR79692
ID AAR79692 standard; peptide; 8 AA.
XX
AC AAR79692;
XX
DT 27-FEB-1996 (first entry)
XX
DE pp60(c-src) kinase phosphorylation site in mouse polyoma middle t Ag.
XX
KW Peptide library; phosphorylation site; protein kinase; substrate;
KW inhibitor; competitor; cellular response; cell cycle control;
KW immune response; transcriptional activation; cell development.
XX
OS Synthetic.
XX
PN WO9518823-A2.
XX
PD 13-JUL-1995.
XX
PF 06-JAN-1995; 95WO-US00147.
XX
PR 07-JAN-1994; 94US-0178570.
XX
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
XX
PI Cantley LC, Songyang Z;
XX
DR WPI; 1995-255036/33.
XX
PT Determn.of amino acid sequence of protein kinase phosphorylation
PT site - by phosphorylation of peptide library and sequencing
PT phospho:peptide(s) formed, also new substrates and their analogues
PT for modulating or detecting protein kinase
XX
PS Example 7; Page 36; 131pp; English.
XX
CC An oriented degenerate peptide library of the amino acid formula
CC AAR79661 was constructed to isolate the amino acid sequences at the
CC phosphorylation sites of a protein kinase eg. protein kinase A,
CC cyclin B/p33(cdc2), src family kinases, etc. Peptides which are
CC phosphorylated are isolated and their amino acid sequences are compared
CC to known substrate/inhibitor peptide sequences for that protein kinase.
CC The peptides AAR79689-R79700 represent phosphorylation sites for the src
CC family kinases pp60(c-src) or pp60(v-src). This peptide sequence is the

CC phosphorylation site in the mouse polyoma middle t antigen at Tyr315.
CC The isolated peptides can be used to screen cpds. for effects on the
CC protein kinase activity, generate antibodies to identify native kinase
CC substrates, or modulate a variety of cellular responses in which protein
CC kinases are involved eg. cell cycle control, immune response,
CC transcriptional activation or cell development.
XX
SQ Sequence 8 AA;

Query Match 47.6%; Score 20; DB 16; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EKKYSP 8
|::| |
Db 1 eeeymp 6

RESULT 9
AAW39531
ID AAW39531 standard; peptide; 8 AA.
XX
AC AAW39531;
XX
DT 11-JUN-1998 (first entry)
XX
DE HIV-1 pol peptide (pos. 184-191) capable of binding to HLA-A*0301.
XX
KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
KW vaccine; immunogenic; major histocompatablilty complex; MHC; B cell;
KW disease; anti-tumour; anti-viral.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO9741440-A1.
XX
PD 06-NOV-1997.
XX
PF 28-APR-1997; 97WO-NL00229.
XX
PR 23-DEC-1996; 96EP-0203670.
PR 26-APR-1996; 96EP-0201145.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
XX
PI Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;
XX
DR WPI; 1997-549891/50.
XX
PT Method of selecting T cell peptide epitope(s) - by measuring the
PT stability of HLA class I-peptide complexes on intact B cells
XX
PS Example 2; Page 62; 109pp; English.
XX
CC Peptides AAW39430-W39734 are used in a novel method for the selection of
CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The
CC method involves the identification of peptide sequences capable of
CC binding to an HLA (human leukocyte antigen) class I molecule and
CC measuring the binding of this epitope peptide to the HLA class I
CC peptide. The stability of binding of the peptide and MHC (major
CC histocompatablilty complex) class I molecule is measured on intact human
CC B cells carrying the MHC molecule at their cell surfaces. The method can
CC be used to select peptide epitopes for generating vaccines against a
CC disease associated with the polypeptide, e.g. cancers or AIDS. The
CC peptide epitopes are especially T-cell peptide epitopes with strong
CC anti-tumour and anti-viral immune responses. Peptides AAW39528-W39547 are
CC conserved human immunodeficiency virus type 1 (HIV-1) pol sequences which
CC are compliant with the HLA-A*0301 binding motif.
XX
SQ Sequence 8 AA;

Query Match 47.6%; Score 20; DB 18; Length 8;
Best Local Similarity 80.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTEKK 5
|||:|
Db 2 lteek 6

RESULT 10
AAY19720
ID AAY19720 standard; Protein; 8 AA.
XX
AC AAY19720;
XX
DT 14-JUL-1999 (first entry)
XX
DE SEQ ID NO 438 from WO9922243.
XX
KW Human secreted protein; cancer; tumour; neurodegenerative disorder;
KW developmental abnormality; fetal deficiency; blood disorder; leukemia;
KW immune system disease; autoimmune disease; hepatic disease;
KW renal disease; lymphoma; inflammation; allergy; ischemic shock;
KW Alzheimer's; cognitive disorder; schizophrenia; prostate disease;
KW obesity; osteoclast; osteoporosis; arthritis; malignancy; testes disease;
KW lung disease; thymus disease; digestive disorder; endocrine disorder;
KW infection; AIDS.
XX
OS Homo sapiens.
XX
PN WO9922243-A1.
XX
PD 06-MAY-1999.
XX
PF 23-OCT-1998; 98WO-US22376.
XX
PR 24-OCT-1997; 97US-0063387.
PR 24-OCT-1997; 97US-0062784.
PR 24-OCT-1997; 97US-0063088.
PR 24-OCT-1997; 97US-0063089.
PR 24-OCT-1997; 97US-0063090.
PR 24-OCT-1997; 97US-0063091.
PR 24-OCT-1997; 97US-0063092.
PR 24-OCT-1997; 97US-0063097.
PR 24-OCT-1997; 97US-0063098.
PR 24-OCT-1997; 97US-0063099.
PR 24-OCT-1997; 97US-0063100.
PR 24-OCT-1997; 97US-0063101.
PR 24-OCT-1997; 97US-0063109.
PR 24-OCT-1997; 97US-0063110.
PR 24-OCT-1997; 97US-0063111.
PR 24-OCT-1997; 97US-0063148.
PR 24-OCT-1997; 97US-0063386.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Brewer LA, Carter KC, Duan DR, Ebner R, Endress GA;
PI Feng P, Florence C, Florence KA, Greene JM, Janat F;
PI Kayw H, Lafleur DW, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Ruben SM, Shi Y, Soppet DR, Wei Y, Young P;
XX
DR WPI; 1999-303069/25.
XX
PT New isolated human genes and the secreted polypeptides they encode
XX
PS Disclosure; Page 508; 546pp; English.
XX
CC The specification describes human secreted proteins. The polynucleotides
CC and their corresponding secreted polypeptides are useful for preventing,
CC treating or ameliorating medical conditions, e.g. by protein or gene
CC therapy. Pathological conditions can also be diagnosed by determining
CC the amount of the polypeptides in a sample or by determining the presence

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CC   of mutations in the polynucleotides. Specific uses are described for each
CC   of the polynucleotides, based on which tissues they are most highly
CC   expressed in, and include developing products for the diagnosis or
CC   treatment of cancer, tumours, neurodegenerative disorders, developmental
CC   abnormalities and fetal deficiencies, blood disorders, leukemias,
CC   diseases of the immune system, autoimmune diseases, hepatic and renal
CC   disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's
CC   and cognitive disorders, schizophrenia, prostate diseases, obesity,
CC   disorders involving osteoclasts such as osteoporosis, arthritis or
CC   malignancies, diseases of testes, lung or thymus, digestive/endocrine
CC   disorders, infections and AIDS. The polypeptides are also useful for
CC   identifying their binding partners.
XX
SQ   Sequence   8 AA;


  Query Match             47.6%;  Score 20;  DB 20;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 4.3e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEKK 5
           |:|||
Db       3 lsekk 7


RESULT  11
AAY57993
ID   AAY57993 standard; peptide; 8 AA.
XX
AC   AAY57993;
XX
DT   23-MAR-2000  (first entry)
XX
DE   Mouse polyoma middle t (Y315) peptide SEQ ID NO:47.
XX
KW   Protein kinase; phosphorylation site; signal transduction.
XX
OS   Mus sp.
XX
PN   US6004757-A.
XX
PD   21-DEC-1999.
XX
PF   06-JAN-1995;   95US-0369643.
XX
PR   07-JAN-1994;   94US-0178570.
XX
PA   (BETH-) BETH ISRAEL HOSPITAL ASSOC.
XX
PI   Cantley LC,  Songyang Z;
XX
DR   WPI; 2000-096301/08.
XX
PT   Peptide substrate for a kinase, useful for determining substrate
PT   specificity -
XX
PS   Example 7; Column 34; 69pp; English.
XX
CC   The present invention describes a substrate for lck comprising a 9 amino
CC   acid peptide (I). Also described is a method of inhibiting kinase
CC   activity of lck by contacting it with (I) in vitro. The peptide is
CC   useful for determining substrate specificity of a protein kinase.
CC   Information on the substrate specificity of protein kinases in signal
CC   transduction would provide an insight into signal transduction
CC   mechanisms and could allow for the design of therapeutic agents. The
CC   present sequence represents a peptide used in the exemplification of
CC   the present invention.
XX
SQ   Sequence   8 AA;


  Query Match             47.6%;  Score 20;  DB 21;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 4.3e+05;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 EKKYSP 8
           |::| |
Db       1 eeeymp 6


RESULT  12
AAR72419
ID   AAR72419 standard; Peptide; 8 AA.
XX
AC   AAR72419;
XX
DT   21-JUN-1995  (first entry)
XX
DE   Recombinant timothy grass allergen Phl pII epitope AS 69-76.
XX
KW   Timothy grass; Phleum pratense; allergen; recombinant; group II/III;
KW   grass; plant; pollen; B-cell; T-cell; epitope; detection; allergy.
XX
OS   Phleum pratense.
XX
PN   WO9423035-A.
XX
PD   13-OCT-1994.
XX
PF   31-MAR-1994;   94WO-AT00039.
XX
PR   01-APR-1993;   93AT-0000672.
XX
PA   (BIOM-) BIOMAY PRODN & HANDELSGES MBH.
XX
PI   Dolecek C,  Kraft D,  Laffer S,  Scheiner O,  Steinberger P;
PI   Valenta R,  Vrtala S;
XX
DR   WPI; 1994-333195/41.
XX
PT   Recombinant timothy grass pollen allergen Phl p II - useful in a
PT   process for the in-vitro detection of Phl p II allergies and for
PT   the treatment of pollen allergies in mammalians
XX
PS   Disclosure; Fig 3; 24pp; German.
XX
CC   A series of synthetic B-cell epitopes (AAR72414-20) generated from the
CC   amino acid sequence (AAR63207) of the timothy grass allergen Phl pII.
CC   The gene (AAQ77731) encodes a protein of 122 a.a. including a 26 a.a.
CC   signal peptide sequence.  This is the first complete recombinant allergen
CC   from the group II/III plant pollen allergens.  The allergen or its
CC   epitopes can be used in the detection of either an allergy in a patient
CC   against the pHl pII allergen or a cellular reaction to the allergen.
CC   Mammalian pollen allergy may be treated using recombinant or synthetic
CC   Phl pII or at least one of its epitopes.
XX
SQ   Sequence   8 AA;


  Query Match             45.2%;  Score 19;  DB 15;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 LTEK 4
           ||||
Db       1 ltek 4


RESULT  13
AAR79693
ID   AAR79693 standard; peptide; 8 AA.
XX
AC   AAR79693;
XX
DT   27-FEB-1996  (first entry)
XX
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DE pp60(c-src) kinase phosphorylation site in hamster polyoma middle t Ag.
XX
KW Peptide library; phosphorylation site; protein kinase; substrate;
KW inhibitor; competitor; cellular response; cell cycle control;
KW immune response; transcriptional activation; cell development.
XX
OS Synthetic.
XX
PN WO9518823-A2.
XX
PD 13-JUL-1995.
XX
PF 06-JAN-1995; 95WO-US00147.
XX
PR 07-JAN-1994; 94US-0178570.
XX
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
XX
PI Cantley LC, Songyang Z;
XX
DR WPI; 1995-255036/33.
XX
PT Determn.of amino acid sequence of protein kinase phosphorylation
PT site - by phosphorylation of peptide library and sequencing
PT phospho:peptide(s) formed, also new substrates and their analogues
PT for modulating or detecting protein kinase
XX
PS Example 7; Page 36; 131pp; English.
XX
CC An oriented degenerate peptide library of the amino acid formula
CC AAR79661 was constructed to isolate the amino acid sequences at the
CC phosphorylation sites of a protein kinase eg. protein kinase A,
CC cyclin B/p33(cdc2), src family kinases, etc. Peptides which are
CC phosphorylated are isolated and their amino acid sequences are compared
CC to known substrate/inhibitor peptide sequences for that protein kinase.
CC The peptides AAR79689-R79700 represent phosphorylation sites for the src
CC family kinases pp60(c-src) or pp60(v-src). This peptide sequence is the
CC phosphorylation site in hamster polyoma middle t antigen at Tyr295.
CC The isolated peptides can be used to screen cpds. for effects on the
CC protein kinase activity, generate antibodies to identify native kinase
CC substrates, or modulate a variety of cellular responses in which protein
CC kinases are involved eg. cell cycle control, immune response,
CC transcriptional activation or cell development.
XX
SQ Sequence 8 AA;

Query Match 45.2%; Score 19; DB 16; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EKKYSP 8
| :| |
Db 1 eneymp 6

RESULT 14
AAW05444
ID AAW05444 standard; Peptide; 8 AA.
XX
AC AAW05444;
XX
DT 24-FEB-1998 (first entry)
XX
DE SH2-binding peptide for Grb2.
XX
KW Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
KW cellular signalling element; cellular structural element; malignancy;
KW protein identification; functional domain; protein screening;
KW cellular signal transduction process; binding peptide.
XX
OS Synthetic.
XX
PN WO9631625-A1.
XX
PD 10-OCT-1996.
XX
PF 04-APR-1996; 96WO-US04454.
XX
PR 03-APR-1996; 96US-0630915.
PR 07-APR-1995; 95US-0417872.
XX
PA (CYTO-) CYTOGEN CORP.
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Fowlkes DM, Hoffman N, Kay BK, Mcconnell SJ, Sparks AB;
XX
DR WPI; 1996-465045/46.
XX
PT Identifying polypeptide(s) having specific functional domain (esp.
PT SH3 domain) - comprises detecting selective binding to recognition
PT unit, regardless of sequence homology
XX
PS Example; Page 92; 174pp; English.
XX
CC AAW05438-W05444 represent Src-homology region 2 (SH2) domain binding
CC peptides. These sequences were used as parts of multivalent recognition
CC unit complexes used in the method of the invention. The method of the
CC invention is for identifying polypeptides containing functional domains
CC of interest, especially Src-homology region 3 (SH3) domains. It
CC comprises contacting a multivalent recognition unit (RU) complex with a
CC number of peptides and identifying polypeptides having a selective
CC binding affinity for the RU complex. The method is based on functional
CC similarities and does not rely on sequence similarities. Prior methods
CC only gave limited success for identifying proteins containing an SH3
CC domain due to the minimal sequence homology among known SH3 proteins.
CC Multivalent RU complexes are particularly suited to screening for
CC polypeptides containing functional domains that are similar to, but not
CC identical in sequence to, the original target functional domain. The new
CC method enables proteins having a common function to be identified.
CC Identification of novel SH3 proteins will be useful for a better
CC understanding of cell growth, malignancy, signal transduction processes,
CC etc. New candidate drugs can be identified, and their specificities
CC (e.g. pharmacological activities) can be assessed using the method of
CC the invention.
XX
SQ Sequence 8 AA;

Query Match 45.2%; Score 19; DB 17; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 KKYSP 8
: |||
Db 4 qnysp 8

RESULT 15
AAY47205
ID AAY47205 standard; Peptide; 8 AA.
XX
AC AAY47205;
XX
DT 01-DEC-1999 (first entry)
XX
DE Immunogenic peptide having a human leukocyte antigen binding motif #1816.
XX
KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
OS Synthetic.
OS Homo sapiens.

XX
PN WO9945954-A1.
XX
PD 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US05039.
XX
PR 13-MAR-1998; 98WO-US05039.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX
DR WPI; 1999-551214/46.
XX
PT New immunogenic peptides with HLA binding motif, useful in treatment
PT and diagnosis of cancers and viral diseases -
XX
PS Claim 1; Page 98; 150pp; English.
XX
CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also
CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
CC response against the antigen from which the peptide is derived.
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
CC normally induced by an antigen in the form of a peptide fragment bound
CC to a HLA molecule, rather than the intact foreign antigen itself, and
CC are particularly important in tumour rejection and in fighting viral
CC infections. The peptides are therefore useful therapeutically to treat
CC or prevent viral infections and cancers in mammals (especially humans)
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
CC They can be administered as vaccines to elicit an immune response in
CC individuals susceptible or otherwise at risk of viral infection or
CC cancer, or used to treat chronic or acute conditions. They are also
CC useful diagnostically, and can be used to induce a cytotoxic T cell
CC response, by contacting a cytotoxic T cell with the peptide e.g. to
CC produce CTLs ex vivo for infusion back into a patient. The
CC polynucleotides encoding the immunogenic peptides are also useful
CC therapeutically and for immunisation as above.
XX
SQ Sequence 8 AA;

Query Match 45.2%; Score 19; DB 20; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 LTEKKY 6
            | ::||
Db      2 lvqeky 7
```

Search completed: December 13, 2001, 11:57:18
Job time: 101 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 11:56:34 ; Search time 22.27 Seconds
(without alignments)
27.364 Million cell updates/sec

Title: US-09-424-080A-2
Perfect score: 11
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 147

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	36.4	8	1	LFSAME	probable msrA lead
2	4	36.4	8	2	A32523	peptidyl-dipeptida
3	4	36.4	8	2	A61348	red pigment-concen
4	4	36.4	8	2	S08996	hypertrehalosemic
5	4	36.4	8	2	B49823	adipokinetic hormo
6	4	36.4	8	2	B44960	neuropeptide Led-C
7	4	36.4	8	2	S15422	adipokinetic hormo
8	4	36.4	8	2	A43976	hypertrehalosemic
9	4	36.4	8	2	B43976	hypertrehalosemic
10	4	36.4	8	2	A33995	adipokinetic hormo
11	4	36.4	8	2	S11545	adipokinetic hormo
12	4	36.4	8	2	A58641	adipokinetic hormo
13	4	36.4	8	2	PH1407	Ig heavy chain V r
14	4	36.4	8	2	E60588	sperm-activating p
15	4	36.4	8	2	F60588	sperm-activating p
16	4	36.4	8	2	G60588	sperm-activating p
17	4	36.4	8	2	B24749	neuropeptide B - b
18	4	36.4	8	2	T10077	hypothetical prote
19	4	36.4	8	2	PC4131	hypothetical prote
20	4	36.4	8	2	PC1002	leucine--tRNA liga
21	4	36.4	8	2	S65647	2-hydroxyglutaryl-
22	4	36.4	8	2	A39308	glycine reductase
23	4	36.4	8	2	T48890	hypothetical prote
24	4	36.4	8	2	A37521	R-phycoerythrin ga
25	4	36.4	8	2	S68802	nitrate reductase
26	4	36.4	8	2	S16324	hypothetical prote
27	4	36.4	8	2	PA0035	protein QA300039 -
28	4	36.4	8	2	PA0032	protein QA300040 -
29	4	36.4	8	2	T10952	hypothetical prote
30	4	36.4	8	2	T14906	hypothetical prote
31	4	36.4	8	2	G33098	205K exoantigen -
32	4	36.4	8	2	A23967	leucopyrokinin - M
33	4	36.4	8	2	S21663	neuropeptide - flo
34	4	36.4	8	2	S66646	cardioacceleratory
35	4	36.4	8	2	D47393	neuropeptide calla
36	4	36.4	8	2	PT0368	Ig gamma chain C r
37	4	36.4	8	2	PT0298	Ig heavy chain CRD
38	4	36.4	8	2	PT0311	Ig heavy chain CRD
39	4	36.4	8	2	PT0323	Ig heavy chain CRD
40	4	36.4	8	2	S10783	enamelin f - bovin
41	4	36.4	8	2	A28719	thymic humoral fac
42	4	36.4	8	2	A42057	fibroblast growth
43	4	36.4	8	2	PH1618	Ig H chain V-D-J r
44	4	36.4	8	2	PN0043	phosphatidylethano
45	4	36.4	8	2	T13818	cytochrome oxidase

ALIGNMENTS

RESULT 1
LFSAME
probable msrA leader peptide - Staphylococcus epidermidis
C;Species: Staphylococcus epidermidis
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: S11157
R;Ross, J.I.; Eady, E.A.; Cove, J.H.; Cunliffe, W.J.; Baumberg, S.; Wootton, J.C.
Mol. Microbiol. 4, 1207-1214, 1990
A;Title: Inducible erythromycin resistance in staphylococci is encoded by a member of
A;Reference number: S11157; MUID:91041730
A;Accession: S11157
A;Molecule type: DNA
A;Residues: 1-8 <ROS>
A;Cross-references: EMBL:X52085; NID:g47000; PIDN:CAA36303.1; PID:g581653
C;Superfamily: probable msrA leader peptide

Query Match 36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 7 L 7

RESULT 2
A32523
peptidyl-dipeptidase A (EC 3.4.15.1) - bovine (fragment)
N;Alternate names: angiotensin I-converting enzyme; peptidyl-dipeptidase I
C;Species: Bos primigenius taurus (cattle)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 11-May-2000
C;Accession: A32523
R;Harris, R.B.
Adv. Exp. Med. Biol. 198, 513-521, 1986
A;Title: Isolation and sequencing of an active-site peptide from angiotensin I-conver
A;Reference number: A32523; MUID:87123961
A;Accession: A32523
A;Molecule type: protein
A;Residues: 1-8 <HAR>
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: alternative splicing; blood pressure control; peptidyldipeptide hydrolase

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 4 L 4

RESULT 3
A61348
red pigment-concentrating hormone - northern shrimp
N;Alternate names: blanching hormone
C;Species: Pandalus borealis (northern shrimp)
C;Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C;Accession: A61348; S07139
R;Fernlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A;Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A;Reference number: A61348; MUID:72228738
A;Accession: A61348
A;Molecule type: protein
A;Residues: 1-8 <FER1>
R;Fernlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A;Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus bore
A;Reference number: S07139; MUID:75054965
A;Accession: S07139
A;Molecule type: protein
A;Residues: 'E',2-8 <FER2>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pi
zed pigment-containing cells.
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutami
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 4
S08996
hypertrehalosemic hormone II - oriental cockroach
N;Alternate names: Pea-CAH-II
C;Species: Blatta orientalis (oriental cockroach)
C;Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C;Accession: S08996
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpor
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A;Reference number: S08995; MUID:90253659
A;Accession: S08996
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 5
B49823
adipokinetic hormone II - American cockroach
N;Alternate names: neuropeptide M-II; periplanetin CC-1
C;Species: Periplaneta americana (American cockroach)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Accession: B49823; A05170
R;Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller,
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
A;Title: Isolation and primary structure of two peptides with cardioacceleratory and
A;Reference number: A49823; MUID:84298179
A;Accession: B49823
A;Molecule type: protein
A;Residues: 1-8 <SCA>
R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr.,
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment
A;Reference number: A90118; MUID:85046530
A;Accession: A05170
A;Molecule type: protein
A;Residues: 'E',2-8 <WIT>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 6
B44960
neuropeptide Led-CC-II - Colorado potato beetle
C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: B44960
R;Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle a
A;Reference number: A44960; MUID:90160053
A;Accession: B44960
A;Molecule type: protein
A;Residues: 1-8 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutam
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimenta

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 7
S15422
adipokinetic hormone - cockchafer
C;Species: Melolontha melolontha (cockchafer)
C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: S15422
R;Gaede, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red
A;Reference number: S15422; MUID:91248100
A;Accession: S15422

A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 8
A43976
hypertrehalosemic hormone - yellow mealworm
C;Species: Tenebrio molitor (yellow mealworm)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 07-May-1999
C;Accession: A43976
R;Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid be
A;Reference number: A43976; MUID:90341081
A;Accession: A43976
A;Molecule type: protein
A;Residues: 1-8 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 9
B43976
hypertrehalosemic hormone - beetle (Zophobas rugipes)
C;Species: Zophobas rugipes
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 07-May-1999
C;Accession: B43976
R;Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid be
A;Reference number: A43976; MUID:90341081
A;Accession: B43976
A;Molecule type: protein
A;Residues: 1-8 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 10
A33995
adipokinetic hormone - black horse fly
C;Species: Tabanus atratus (black horse fly)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997
C;Accession: A33995
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhan
Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotre
A;Reference number: A33995; MUID:90046758
A;Accession: A33995
A;Molecule type: protein
A;Residues: 1-8 <JAF>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 11
S11545
adipokinetic hormone - nestling-sucking blowfly
C;Species: Protophormia terraenovae (nestling-sucking blowfly)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 31-Oct-1997
C;Accession: S11545
R;Gaede, G.; Wilps, H.; Kellner, R.
Biochem. J. 269, 309-313, 1990
A;Title: Isolation and structure of a novel charged member of the red-pigment-concent
erraenovae (Diptera).
A;Reference number: S11545; MUID:90351345
A;Accession: S11545
A;Molecule type: protein
A;Residues: 1-8 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 12
A58641
adipokinetic hormone - dor beetle
C;Species: Geotrupes stercorosus (dor beetle)
C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: A58641
R;Gaede, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red
A;Reference number: S15422; MUID:91248100
A;Accession: A58641
A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 13
PH1407
Ig heavy chain V region (clone micro m+ 46-6 PCR) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PH1407
R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta
J. Exp. Med. 176, 1209-1214, 1992
A;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
ia virus.
A;Reference number: PH1403; MUID:93018837
A;Accession: PH1407
A;Molecule type: DNA
A;Residues: 1-8 <SHI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 5 L 5

RESULT 14
E60588
sperm-activating peptide a - sea urchin (Pseudoboletia maculata)
N;Alternate names: speract homolog
C;Species: Pseudoboletia maculata
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C;Accession: E60588
R;Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguc
Comp. Biochem. Physiol. B 94, 739-751, 1989
A;Title: A halogenated amino acid-containing sperm activating peptide and its related pe
otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.
A;Reference number: A60527
A;Accession: E60588
A;Molecule type: protein
A;Residues: 1-8 <YOS>
C;Superfamily: unassigned animal peptides

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 4 L 4

RESULT 15
F60588
sperm-activating peptide b - sea urchin (Pseudoboletia maculata)
N;Alternate names: speract homolog
C;Species: Pseudoboletia maculata
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C;Accession: F60588
R;Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yama
Comp. Biochem. Physiol. B 94, 739-751, 1989
A;Title: A halogenated amino acid-containing sperm activating peptide and its related
otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.
A;Reference number: A60527
A;Accession: F60588
A;Molecule type: protein
A;Residues: 1-8 <YOS>
C;Superfamily: unassigned animal peptides

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 4 L 4

Search completed: December 13, 2001, 11:56:34
Job time: 57 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:45:38 ; Search time 22.81 Seconds
(without alignments)
26.716 Million cell updates/sec

Title: US-09-424-080A-2
Perfect score: 11
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	36.4	3	2	PQ0010	angiotensin-conver
2	4	36.4	3	2	T13892	cytochrome-c oxida
3	4	36.4	4	2	S18401	thyroglobulin - do
4	4	36.4	4	2	A32039	tyrosine-melanocyt
5	4	36.4	4	2	A48360	gamma subunit of P
6	4	36.4	4	2	B43848	cell surface adhes
7	4	36.4	4	2	I40505	hypothetical prote
8	4	36.4	4	2	T46627	hypothetical prote
9	4	36.4	4	2	I38888	COI intron 16 prot
10	4	36.4	4	2	A35779	neuropeptide Antho
11	4	36.4	4	2	PT0240	Ig heavy chain CRD
12	4	36.4	4	2	A53284	T-cell receptor be
13	4	36.4	4	2	PT0645	T-cell receptor be
14	4	36.4	4	2	PT0721	T-cell receptor be
15	4	36.4	4	2	S47552	ubiquitin - rat
16	4	36.4	4	2	A26209	protein-glutamine
17	4	36.4	5	1	HOROHA	proctolin - Americ
18	4	36.4	5	2	JN0860	peptidyl-dipeptida
19	4	36.4	5	2	C41225	copper resistance
20	4	36.4	5	2	E42364	flagellar protein
21	4	36.4	5	2	B22565	R-phycoerythrin al
22	4	36.4	5	2	PQ0009	angiotensin-conver
23	4	36.4	5	2	S55237	zinc-binding prote
24	4	36.4	5	2	A60803	neuropeptide - sea
25	4	36.4	5	2	B61445	Leu-enkephalin - b
26	4	36.4	5	2	A60411	proctolin - Atlant
27	4	36.4	5	2	S53595	hypothetical prote
28	4	36.4	5	2	PT0278	Ig heavy chain CRD
29	4	36.4	5	2	D44823	synaptosomal-assoc
30	4	36.4	5	2	PT0624	T-cell receptor be
31	4	36.4	5	2	PT0625	T-cell receptor be
32	4	36.4	5	2	PT0713	T-cell receptor be
33	4	36.4	5	2	G44817	27.5 kda structura
34	4	36.4	5	2	I44817	27.5K structural p
35	4	36.4	5	2	E44817	27.5K structural p
36	4	36.4	5	2	C44817	28.5K structural p
37	4	36.4	5	2	A44817	28K structural pro
38	4	36.4	5	2	B44817	34.5K structural p
39	4	36.4	5	2	D44817	35K structural pro
40	4	36.4	5	2	S69237	surface protein te
41	4	36.4	5	4	A58728	serrawettin W2 - S
42	4	36.4	6	2	A35890	RNA-directed DNA p
43	4	36.4	6	2	B34835	dnaA protein - Pse
44	4	36.4	6	2	A60986	N-formyl oligopept
45	4	36.4	6	2	T11779	phosphoglycerate t

ALIGNMENTS

RESULT 1
PQ0010
angiotensin-converting enzyme inhibitor (FLP-3) - common fig
N;Alternate names: ficus latex peptide 3
C;Species: Ficus carica (common fig)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C;Accession: PQ0010
R;Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A;Reference number: PQ0008
A;Accession: PQ0010
A;Molecule type: protein
A;Residues: 1-3 <MAR>
A;Experimental source: latex
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 36.4%; Score 4; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 1 L 1

RESULT 2
T13892
cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (f
C;Species: mitochondrion Lampetra fluviatilis (river lamprey)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T13892
R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the
A;Reference number: Z17775; MUID:97398704
A;Accession: T13892
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3 <DEL>
A;Cross-references: EMBL:Y09528; NID:g2340016; PIDN:CAA70721.1; PID:g4379123
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 36.4%; Score 4; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 L 1
          |
Db      3 L 3
```

RESULT 3
S18401
thyroglobulin - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 19-Mar-1997 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: S18401
R;Donda, A.; Vassart, G.; Christophe, D.
Biochim. Biophys. Acta 1090, 235-237, 1991
A;Title: Isolation and characterization of the canine thyroglobulin gene promoter regior
A;Reference number: S18401; MUID:92031697
A;Accession: S18401
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <DON>
A;Cross-references: GB:S61184; NID:g237714; PIDN:AAB20127.1; PID:g237715
C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homol
C;Keywords: duplication; iodine; thyroid gland; thyroid hormone biosynthesis

```
  Query Match             36.4%;  Score 4;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      3 L 3
```

RESULT 4
A32039
tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C;Accession: A32039
R;Horvath, A.; Kastin, A.J.
J. Biol. Chem. 264, 2175-2179, 1989
A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor
A;Reference number: A32039; MUID:89123285
A;Accession: A32039
A;Molecule type: protein
A;Residues: 1-4 <HOR>
A;Experimental source: brain
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end
F;4/Modified site: amidated carboxyl end (Gly) #status experimental

```
  Query Match             36.4%;  Score 4;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      3 L 3
```

RESULT 5
A48360
gamma subunit of Protein A - Methylosinus trichosporium (fragment)
C;Species: Methylosinus trichosporium
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: A48360
R;Cardy, D.L.; Laidler, V.; Salmond, G.P.; Murrell, J.C.
Arch. Microbiol. 156, 477-483, 1991
A;Title: The methane monooxygenase gene cluster of Methylosinus trichosporium: cloning a
A;Reference number: A48360; MUID:92153031
A;Contents: OB3b
A;Accession: A48360
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <CAR>
A;Cross-references: GB:S81887; NID:g245213; PIDN:AAB21391.1; PID:g245214
A;Note: sequence extracted from NCBI backbone (NCBIN:81887, NCBIP:81912)

```
  Query Match             36.4%;  Score 4;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 L 2
```

RESULT 6
B43848
cell surface adhesin for heparan sulfate, 60K - Staphylococcus aureus (fragment)
C;Species: Staphylococcus aureus
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1995
C;Accession: B43848
R;Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
Infect. Immun. 60, 899-906, 1992
A;Title: Binding of heparan sulfate to Staphylococcus aureus.
A;Reference number: A43848; MUID:92176005
A;Accession: B43848
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <LIA>
A;Note: sequence extracted from NCBI backbone (NCBIP:85444)

```
  Query Match             36.4%;  Score 4;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 L 2
```

RESULT 7
I40505
hypothetical protein 3 (4 aa) - Bacillus stearothermophilus
C;Species: Bacillus stearothermophilus
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
C;Accession: I40505
R;Waye, M.M.; Winter, G.
Eur. J. Biochem. 158, 505-510, 1986
A;Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA s
A;Reference number: I40503; MUID:86274732
A;Accession: I40505
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 <RES>
A;Cross-references: EMBL:X04193; NID:g40233; PIDN:CAA27783.1; PID:g580944

```
  Query Match             36.4%;  Score 4;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 L 2
```

RESULT 8
T46627
hypothetical protein c4 - loblolly pine
C;Species: Pinus taeda (loblolly pine)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C;Accession: T46627
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
submitted to the EMBL Data Library, July 1995
A;Description: Cloning of a chitinase homolog which lacks chitin binding sites and is dc
A;Reference number: Z23105
A;Accession: T46627
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-4 <CHA>
A;Cross-references: EMBL:U31309; NID:g974285; PID:g974292
A;Experimental source: strain s6PT2xs6PT3; 8 month seedlings

Query Match 36.4%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 3 L 3

RESULT 9
I38888
COI intron 16 protein - Podospora anserina mitochondrion
C;Species: mitochondrion Podospora anserina
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Dec-1999
C;Accession: I38888
R;Cummings, D.J.; Michel, F.; McNally, K.L.
Curr. Genet. 16, 381-406, 1989
A;Title: DNA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit I mi
A;Reference number: A48327; MUID:90124722
A;Accession: I38888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <CUM>
A;Cross-references: GB:X55026; GB:M30937; GB:M61734
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC3
C;Keywords: mitochondrion

Query Match 36.4%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 10
A35779
neuropeptide Antho-RNamide - sea anemone (Anthopleura elegantissima)
C;Species: Anthopleura elegantissima
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 08-Dec-1995
C;Accession: A35779
R;Grimmelikhuijzen, C.J.P.; Rinehart, K.L.; Jacob, E.; Graff, D.; Reinscheid, R.K.; Noth
Proc. Natl. Acad. Sci. U.S.A. 87, 5410-5414, 1990
A;Title: Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea anemone ne
A;Reference number: A35779; MUID:90319122
A;Accession: A35779
A;Molecule type: protein
A;Residues: 1-4 <GRI>
C;Comment: The L-3-phenyllactyl blocking group probably arises from an amino-terminal ph
C;Keywords: amidated carboxyl end; neuropeptide; phenyllactylation
F;1/Modified site: L-3-phenyllactic acid (Phe) #status experimental
F;4/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 11
PT0240
Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0240
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A;Reference number: PT0222; MUID:91108337
A;Accession: PT0240
A;Molecule type: DNA
A;Residues: 1-4 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 36.4%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 4 L 4

RESULT 12
A53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity an
A;Reference number: A53284; MUID:91342695
A;Accession: A53284
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <HAR>
A;Cross-references: GB:S60737; NID:g233916; PIDN:AAB19517.1; PID:g233917
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60739)
C;Keywords: T-cell receptor

Query Match 36.4%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 13
PT0645
T-cell receptor beta chain V-D-J region (111-1AI) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0645; PT0626
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0645
A;Status: translation not shown

A;Molecule type: mRNA
A;Residues: 1-4 <FEE>
A;Experimental source: newborn thymus, strain BALB/c, 111-1AI
A;Accession: PT0626
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, 120-2CJ
C;Keywords: T-cell receptor

Query Match 36.4%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 4 L 4

RESULT 14
PT0721
T-cell receptor beta chain V-D-J region (140-2K) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0721
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0721
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 36.4%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 3 L 3

RESULT 15
S47552
ubiquitin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
C;Accession: S47552
R;Hubbard, M.J.; Carne, A.
Biochim. Biophys. Acta 1200, 191-196, 1994
A;Title: Differential feeding-related regulation of ubiquitin and calbindin(9kDa) in rat
A;Reference number: S47552; MUID:94304928
A;Accession: S47552
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <HUB>

Query Match 36.4%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 1 L 1

Search completed: December 13, 2001, 10:45:38
Job time: 58 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:50:49 ; Search time 12.78 Seconds
(without alignments)
22.951 Million cell updates/sec

Title: US-09-424-080A-2
Perfect score: 11
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	36.4	4	1	FAR3_HIRME	P42562 hirudo medi
2	4	36.4	4	1	FLRF_HIRME	P42561 hirudo medi
3	4	36.4	5	1	AL14_CARMA	P81817 carcinus ma
4	4	36.4	5	1	PRCT_PERAM	P01373 periplaneta
5	4	36.4	6	1	ACPH_RABIT	P25154 oryctolagus
6	4	36.4	6	1	TMOF_SARBU	P41495 sarcophaga
7	4	36.4	6	1	TRPI_PSEPU	P36414 pseudomonas
8	4	36.4	6	1	VP19_HSV1K	P23210 herpes simp
9	4	36.4	7	1	ALL2_CARMA	P81805 carcinus ma
10	4	36.4	7	1	ALL3_CARMA	P81806 carcinus ma
11	4	36.4	7	1	ALL4_CARMA	P81807 carcinus ma
12	4	36.4	7	1	ALL5_CARMA	P81808 carcinus ma
13	4	36.4	7	1	ALL7_CYDPO	P82158 cydia pomon
14	4	36.4	7	1	CARP_MYTED	P10420 mytilus edu
15	4	36.4	7	1	CCF1_ENTFA	P20104 enterococcu
16	4	36.4	7	1	CIA_ENTFA	P11932 enterococcu
17	4	36.4	7	1	FAR1_HELTI	P41871 helisoma tr
18	4	36.4	7	1	FAR1_PROCL	P38499 procambarus
19	4	36.4	7	1	FAR2_ASCSU	P31890 ascaris suu
20	4	36.4	7	1	FAR2_PROCL	P38498 procambarus
21	4	36.4	7	1	GFRP_MOUSE	P99025 mus musculu
22	4	36.4	7	1	MNP1_LEPDE	P42984 leptinotars
23	4	36.4	7	1	MYOM_APLCA	P15513 aplysia cal
24	4	36.4	7	1	UF03_MOUSE	P38641 mus musculu
25	4	36.4	7	1	UN06_PINPS	P81675 pinus pinas
26	4	36.4	8	1	AKH_MELML	P25423 melolontha
27	4	36.4	8	1	AKH_TABAT	P14595 tabanus atr
28	4	36.4	8	1	AL12_CARMA	P81815 carcinus ma
29	4	36.4	8	1	AL15_CARMA	P81818 carcinus ma
30	4	36.4	8	1	AL16_CARMA	P81819 carcinus ma
31	4	36.4	8	1	AL17_CARMA	P81820 carcinus ma
32	4	36.4	8	1	AL18_CARMA	P81821 carcinus ma
33	4	36.4	8	1	ALL1_CYDPO	P82152 cydia pomon
34	4	36.4	8	1	ALL3_CYDPO	P82154 cydia pomon
35	4	36.4	8	1	ALL4_CALVO	P41840 calliphora
36	4	36.4	8	1	ALL4_CYDPO	P82155 cydia pomon
37	4	36.4	8	1	ALL5_CYDPO	P82156 cydia pomon
38	4	36.4	8	1	ALL6_CYDPO	P82157 cydia pomon
39	4	36.4	8	1	ALL7_CARMA	P81809 carcinus ma
40	4	36.4	8	1	ALL8_CARMA	P81811 carcinus ma
41	4	36.4	8	1	ALL9_CARMA	P81812 carcinus ma
42	4	36.4	8	1	CAD1_ENTFA	P13268 enterococcu
43	4	36.4	8	1	COXG_RAT	P80430 rattus norv
44	4	36.4	8	1	CPD1_ENTFA	P13269 enterococcu
45	4	36.4	8	1	NPB_BOVIN	P15507 bos taurus

ALIGNMENTS

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RESULT   1
FAR3_HIRME
ID   FAR3_HIRME     STANDARD;      PRT;     4 AA.
AC   P42562;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FMRFAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.
OS   Hirudo medicinalis (Medicinal leech).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX   NCBI_TaxID=6421;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  598 MW;  69D4073B30000000 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       2 L 2


RESULT   2
FLRF_HIRME
ID   FLRF_HIRME     STANDARD;      PRT;     4 AA.
AC   P42561;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FLRFAMIDE.
OS   Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX   NCBI_TaxID=6421, 27815;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=H.medicinalis;
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=H.trivolvis; TISSUE=Kidney;
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RX   MEDLINE=94286417; PubMed=7912428;
RA   Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT   "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT   trivolvis.";
RL   Peptides 15:31-36(1994).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  582 MW;  69D40729A0000000 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       2 L 2


RESULT   3
AL14_CARMA
ID   AL14_CARMA     STANDARD;      PRT;      5 AA.
AC   P81817;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 14.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       5       5       AMIDATION (POTENTIAL).
SQ   SEQUENCE   5 AA;  586 MW;  672879D5AB300000 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       5 L 5


RESULT   4
PRCT_PERAM
ID   PRCT_PERAM     STANDARD;      PRT;      5 AA.
AC   P01373;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   PROCTOLIN.
OS   Periplaneta americana (American cockroach),
OS   Limulus polyphemus (Atlantic horseshoe crab), and
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blattoidea; Blattidae; Periplaneta.
OX   NCBI_TaxID=6978, 6850, 6759;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=P.americana;
RX   MEDLINE=76074708; PubMed=576;
RA   Starratt A.N., Brown B.E.;
RT   "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT   in insects.";
RL   Life Sci. 17:1253-1256(1975).
RN   [2]
RP   BIOLOGICAL SOURCE.
RC   SPECIES=P.americana;
RX   MEDLINE=81225865; PubMed=6113690;
RA   O'Shea M., Adams M.E.;
RT   "Pentapeptide (proctolin) associated with an identified neuron.";
RL   Science 213:567-569(1981).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=L.polyphemus;
RX   MEDLINE=90287800; PubMed=2356151;
RA   Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA   Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA   Shabanowitz J.;
RT   "Identification of proctolin in the central nervous system of the
RT   horseshoe crab, Limulus polyphemus.";
RL   Peptides 11:205-211(1990).
RN   [4]
RP   SEQUENCE.
RC   SPECIES=C.maenas;
RX   MEDLINE=86232789; PubMed=2872661;
RA   Stangier J., Dircksen H., Keller R.;
RT   "Identification and immunocytochemical localization of proctolin in
RT   pericardial organs of the shore crab, Carcinus maenas.";
RL   Peptides 7:67-72(1986).
CC   -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
CC       MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC   -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC       THE CRAB PERICARDIAL ORGANS.
DR   PIR; A01644; HOROHA.
DR   PIR; A60411; A60411.
KW   Neuropeptide.
SQ   SEQUENCE   5 AA;  649 MW;  71B7673B44600000 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       3 L 3


RESULT   5
ACPH_RABIT
ID   ACPH_RABIT     STANDARD;      PRT;      6 AA.
AC   P25154;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   ACYLAMINO-ACID-RELEASING ENZYME (EC 3.4.19.1) (ACYL-PEPTIDE HYDROLASE)
DE   (APH) (ACYLAMINOACYL-PEPTIDASE) (FRAGMENT).
GN   APEH.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Muscle;
RX   MEDLINE=92222120; PubMed=1807161;
RA   Krishna R.G., Chin C.C.Q., Wold F.;
RT   "N-terminal sequence analysis of N alpha-acetylated proteins after
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RT   unblocking with N-acylaminoacyl-peptide hydrolase.";
RL   Anal. Biochem. 199:45-50(1991).
CC   -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC       TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC       AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC       IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC   -!- CATALYTIC ACTIVITY: ACYLAMINOACYL-PEPTIDE + H(2)O = ACYLAMINO
CC       ACID + PEPTIDE.
CC   -!- SUBUNIT: HOMOTETRAMER.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C; ALSO KNOWN AS THE
CC       PROLYL OLIGOPEPTIDASE FAMILY.
DR   MEROPS; S09.004; -.
DR   InterPro; IPR002471; Prol_endopep_ser.
DR   PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW   Hydrolase; Acetylation.
FT   MOD_RES       1       1       ACETYLATION.
FT   NON_TER       6       6
SQ   SEQUENCE   6 AA;  775 MW;  6732D6C40B16F000 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      6 L 6


RESULT   6
TMOF_SARBU
ID   TMOF_SARBU     STANDARD;      PRT;      6 AA.
AC   P41495;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   TRYPSIN-MODULATING OOSTATIC FACTOR (TMOF).
OS   Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Oestroidea; Sarcophagidae; Sarcophaga.
OX   NCBI_TaxID=7385;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Ovary;
RX   MEDLINE=94211930; PubMed=8159807;
RA   Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
RA   de Loof A.;
RT   "Sequencing and characterization of trypsin modulating oostatic
RT   factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
RT   (Sarcophaga) bullata.";
RL   Regul. Pept. 50:61-72(1994).
CC   -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
CC       IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CC       CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
CC       DEVELOPMENT.
CC   -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
CC       EPITHELIUM AFTER A BLOOD MEAL.
KW   Hormone.
SQ   SEQUENCE   6 AA;  695 MW;  61E72451B7642000 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      5 L 5


RESULT   7
TRPI_PSEPU
ID   TRPI_PSEPU     STANDARD;      PRT;      6 AA.
AC   P36414;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   TRPBA OPERON TRANSCRIPTIONAL ACTIVATOR (FRAGMENT).
GN   TRPI.
OS   Pseudomonas putida.
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=303;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PPG1 C1S;
RX   MEDLINE=89335826; PubMed=2503057;
RA   Eberly L., Crawford I.P.;
RT   "DNA sequence of the tryptophan synthase genes of Pseudomonas
RT   putida.";
RL   Biochimie 71:521-531(1989).
CC   -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
CC       THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
CC       INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
CC       TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC   -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC       REGULATORS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X13299; CAA31660.1; -.
DR   InterPro; IPR000847; HTH_LysR.
DR   PROSITE; PS00044; HTH_LYSR_FAMILY; PARTIAL.
KW   Tryptophan biosynthesis; Transcription regulation; Activator;
KW   DNA-binding.
FT   NON_TER       6       6
SQ   SEQUENCE   6 AA;  683 MW;  77672AA1EDD6F000 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      5 L 5


RESULT   8
VP19_HSV1K
ID   VP19_HSV1K     STANDARD;      PRT;      6 AA.
AC   P23210;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   01-DEC-1992 (Rel. 24, Last annotation update)
DE   CAPSID ASSEMBLY AND DNA MATURATION PROTEIN (VIRION PROTEIN UL38)
DE   (CAPSID PROTEIN VP19C) (FRAGMENT).
GN   UL38.
OS   Herpes simplex virus (type 1 / strain KOS).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Simplexvirus.
OX   NCBI_TaxID=10306;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91101287; PubMed=1846198;
RA   Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
RA   Silverstein S., Wagner E.K.;
RT   "Analysis of the herpes simplex virus type 1 promoter controlling the
RT   expression of UL38, a true late gene involved in capsid assembly.";
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RL   J. Virol. 65:769-786(1991).
CC   -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
CC       EMBEDDED. BINDS DNA.
CC   -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M57646; AAA45830.1; -.
KW   Capsid assembly; Coat protein; DNA-binding.
FT   NON_TER       6      6
SQ   SEQUENCE   6 AA;  703 MW;  67376451A336F000 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       6 L 6


RESULT   9
ALL2_CARMA
ID   ALL2_CARMA     STANDARD;      PRT;     7 AA.
AC   P81805;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 2.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       7      7       AMIDATION (POTENTIAL).
SQ   SEQUENCE   7 AA;  770 MW;  672879CDCB5DDB70 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       7 L 7


RESULT  10
ALL3_CARMA
ID   ALL3_CARMA     STANDARD;      PRT;     7 AA.
AC   P81806;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 3.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Multigene family.
SQ   SEQUENCE   7 AA;  796 MW;  672879CDCB476B70 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       7 L 7


RESULT  11
ALL4_CARMA
ID   ALL4_CARMA     STANDARD;      PRT;     7 AA.
AC   P81807;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 4.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Multigene family.
SQ   SEQUENCE   7 AA;  782 MW;  672879CDCB476AC0 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       7 L 7


RESULT  12
ALL5_CARMA
ID   ALL5_CARMA     STANDARD;      PRT;     7 AA.
AC   P81808;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
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DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 5.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       7      7       AMIDATION.
SQ   SEQUENCE   7 AA;  781 MW;  672879CDCB476420 CRC64;


  Query Match           36.4%;  Score 4;  DB 1;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 L 7


RESULT  13
ALL7_CYDPO
ID   ALL7_CYDPO     STANDARD;      PRT;     7 AA.
AC   P82158;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CYDIASTATIN 7.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       7      7       AMIDATION.
SQ   SEQUENCE   7 AA;  873 MW;  672879CABB569350 CRC64;


  Query Match           36.4%;  Score 4;  DB 1;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 L 7


RESULT  14
CARP_MYTED
ID   CARP_MYTED     STANDARD;      PRT;     7 AA.
AC   P10420;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   01-MAR-1989 (Rel. 10, Last annotation update)
DE   CATCH-RELAXING PEPTIDE (CARP).
OS   Mytilus edulis (Blue mussel).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
OC   Mytiloidea; Mytilidae; Mytilus.
OX   NCBI_TaxID=6550;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=88052022; PubMed=3676797;
RA   Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA   Muneoka Y.;
RT   "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL   Brain Res. 422:374-376(1987).
CC   -!- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)
CC       AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS
CC       RETRACTOR MUSCLE.
DR   PIR; A29342; ECMUCR.
KW   Hormone; Amidation.
FT   MOD_RES       7      7       AMIDATION.
SQ   SEQUENCE   7 AA;  831 MW;  67340726876690B0 CRC64;


  Query Match           36.4%;  Score 4;  DB 1;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      5 L 5


RESULT  15
CCF1_ENTFA
ID   CCF1_ENTFA     STANDARD;      PRT;     7 AA.
AC   P20104;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-FEB-1991 (Rel. 17, Last annotation update)
DE   SEX PHEROMONE CCF10.
OS   Enterococcus faecalis (Streptococcus faecalis).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC   Enterococcus.
OX   NCBI_TaxID=1351;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=89008313; PubMed=3139658;
RA   Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA   Adsit J.C., Dunny G.M., Suzuki A.;
RT   "Structure of cCF10, a peptide sex pheromone which induces
RT   conjugative transfer of the Streptococcus faecalis tetracycline
RT   resistance plasmid, pCF10.";
RL   J. Biol. Chem. 263:14574-14578(1988).
CC   -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC       HEMOLYSIN PLASMID PCF10.
DR   PIR; A30812; A30812.
KW   Pheromone.
SQ   SEQUENCE   7 AA;  790 MW;  72C9D2C731B2C740 CRC64;


  Query Match           36.4%;  Score 4;  DB 1;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


Search completed: December 13, 2001, 10:50:49
Job time: 308 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:50:30 ; Search time 35.74 Seconds
(without alignments)
32.741 Million cell updates/sec

Title: US-09-424-080A-2
Perfect score: 11
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	36.4	4	11	Q08433	Q08433 rattus norv
2	4	36.4	6	4	Q08720	Q08720 homo sapien
3	4	36.4	6	10	P82541	P82541 spinacia ol
4	4	36.4	7	2	Q54248	Q54248 streptomyce
5	4	36.4	7	2	O07354	O07354 synechococc
6	4	36.4	7	2	O50556	O50556 actinobacil
7	4	36.4	7	4	Q15897	Q15897 homo sapien
8	4	36.4	7	8	P92421	P92421 psathyrosta
9	4	36.4	7	8	P92385	P92385 hordeum mar
10	4	36.4	7	8	P92210	P92210 agropyron c
11	4	36.4	7	8	P92214	P92214 amblyopyrum
12	4	36.4	7	8	P92218	P92218 australopyr
13	4	36.4	7	8	P92221	P92221 bromus iner
14	4	36.4	7	8	P92226	P92226 crithopsis
15	4	36.4	7	8	P92372	P92372 haynaldia v
16	4	36.4	7	8	P92381	P92381 hordeum bra
17	4	36.4	7	8	P92387	P92387 henrardia p
18	4	36.4	7	8	P92390	P92390 heteranthel
19	4	36.4	7	8	P92393	P92393 hordeum vul
20	4	36.4	7	8	P92425	P92425 pseudoroegn
21	4	36.4	7	8	P92427	P92427 peridictyon
22	4	36.4	7	8	P92430	P92430 aegilops ta
23	4	36.4	7	8	P92442	P92442 taeniatheru
24	4	36.4	7	8	P92440	P92440 thinopyrum
25	4	36.4	7	8	Q95945	Q95945 saccharomyc
26	4	36.4	7	8	P92403	P92403 lophopyrum
27	4	36.4	7	8	O98866	O98866 spinacia ol
28	4	36.4	7	8	O99182	O99182 gnatholebia
29	4	36.4	7	10	P93233	P93233 lycopersico
30	4	36.4	7	10	Q9C5B3	Q9c5b3 arabidopsis
31	4	36.4	7	11	Q63668	Q63668 rattus norv
32	4	36.4	7	11	Q63480	Q63480 rattus norv
33	4	36.4	7	12	Q66113	Q66113 cherry leaf
34	4	36.4	7	12	Q66205	Q66205 porcine tra
35	4	36.4	7	12	Q9YQ10	Q9yq10 porcine tra
36	4	36.4	7	13	O42564	O42564 fugu rubrip
37	4	36.4	8	2	Q56429	Q56429 thermus aqu
38	4	36.4	8	2	P72279	P72279 rhodococcus
39	4	36.4	8	2	Q45889	Q45889 clostridium
40	4	36.4	8	2	O85406	O85406 coxiella bu
41	4	36.4	8	2	O87471	O87471 haemophilus
42	4	36.4	8	2	P77556	P77556 escherichia
43	4	36.4	8	2	Q51594	Q51594 escherichia
44	4	36.4	8	2	Q9ZIE9	Q9zie9 neisseria m
45	4	36.4	8	13	Q9PS69	Q9ps69 gallus gall

ALIGNMENTS

RESULT 1
Q08433
ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE, MICROSOMAL (EC 2.4.1.17) (UDPGT)
DE (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUNN;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCORONOSIDE.
CC -!- SUBCELLULAR LOCATION: MICROSOME.
DR EMBL; S38636; AAB19259.1; -.
KW Transferase; Glycosyltransferase; Microsome; Multigene family.
FT NON_TER 1 1
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 36.4%; Score 4; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 3 L 3

```
RESULT   2
Q08720
ID   Q08720      PRELIMINARY;    PRT;    6 AA.
AC   Q08720;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Y PROTEIN (FRAGMENT).
GN   CREB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93010691; PubMed=1396344;
RA   Waeber G., Habener J.F.;
RT   "Novel testis germ cell-specific transcript of the CREB gene contains
RT   an alternatively spliced exon with multiple in-frame stop codons.";
RL   Endocrinology 131:2010-2015(1992).
DR   EMBL; X68994; CAA48780.1; -.
FT   NON_TER       1      1
FT   NON_TER       6      6
SQ   SEQUENCE   6 AA;  695 MW;  67272EB9C735D000 CRC64;

  Query Match             36.4%;  Score 4;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       2 L 2


RESULT   3
P82541
ID   P82541      PRELIMINARY;      PRT;    6 AA.
AC   P82541;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CHLOROPLAST 30S RIBOSOMAL PROTEIN S19 BETA (FRAGMENT).
OS   Spinacia oleracea (Spinach).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX   NCBI_TaxID=3562;
RN   [1]
RP   SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC   STRAIN=CV. ALWARO; TISSUE=LEAF;
RX   MEDLINE=20435797; PubMed=10874039;
RA   Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT   "The plastid ribosomal proteins. Identification of all the proteins in
RT   the small subunit of an organelle ribosome (chloroplast).";
RL   J. Biol. Chem. 37:28455-28465(2000).
CC   -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC   -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC   -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC   -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
CC   -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
CC       FORM IS THE MINOR BASIC FORM.
CC   -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
CC   -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR   InterPro; IPR002222; Ribosomal_S19.
DR   Pfam; PF00203; Ribosomal_S19; PARTIAL.
DR   PRINTS; PR00975; RIBOSOMALS19; PARTIAL.
DR   PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW   Ribosomal protein; Chloroplast; rRNA-binding.
FT   NON_TER       6      6
SQ   SEQUENCE   6 AA;  732 MW;  63333735A411C000 CRC64;

  Query Match             36.4%;  Score 4;  DB 10;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       4 L 4


RESULT   4
Q54248
ID   Q54248      PRELIMINARY;      PRT;    7 AA.
AC   Q54248;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE   SECY & ADK GENES (FRAGMENT).
GN   RPLO.
OS   Streptomyces griseus.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1911;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=N2-3-11;
RA   Poehling S., Piepersberg W., Wehmeier U.F.;
RL   Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X95915; CAA65160.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  760 MW;  72C72B01B2D1B2A0 CRC64;

  Query Match             36.4%;  Score 4;  DB 2;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       6 L 6


RESULT   5
O07354
ID   O07354      PRELIMINARY;      PRT;    7 AA.
AC   O07354;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   NIFK (FRAGMENT).
GN   NIFK.
OS   Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothece PCC 8801).
OC   Bacteria; Cyanobacteria; Chroococcales; Cyanothece.
OX   NCBI_TaxID=41431;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RF-1;
RA   Chen H.M.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF003700; AAC35193.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  849 MW;  7412C72AA9D5B030 CRC64;

  Query Match             36.4%;  Score 4;  DB 2;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       5 L 5
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```
RESULT   6
O50556
ID   O50556      PRELIMINARY;      PRT;     7 AA.
AC   O50556;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   GLYA (FRAGMENT).
GN   GLYA.
OS   Actinobacillus actinomycetemcomitans (Haemophilus
OS   actinomycetemcomitans).
OC   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC   Actinobacillus.
OX   NCBI_TaxID=714;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 33384;
RX   MEDLINE=96355846; PubMed=8751884;
RA   Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
RA   Kraig E.;
RT   "cis Elements and trans factors are both important in strain-specific
RT   regulation of the leukotoxin gene in Actinobacillus
RT   actinomycetemcomitans.";
RL   Infect. Immun. 64:3451-3460(1996).
DR   EMBL; U51862; AAB88721.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  832 MW;  6DCB42D767340420 CRC64;


  Query Match             36.4%;  Score 4;  DB 2;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      3 L 3


RESULT   7
Q15897
ID   Q15897      PRELIMINARY;      PRT;     7 AA.
AC   Q15897;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   (CLONE XP6A11A) (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA   Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA   Caskey C.T.H.;
RL   Hum. Mol. Genet. 0:0-0(0).
DR   EMBL; L32077; AAA73887.1; -.
FT   NON_TER       1      1
FT   NON_TER       7      7
SQ   SEQUENCE   7 AA;  814 MW;  672B1DD3372046B0 CRC64;


  Query Match             36.4%;  Score 4;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      3 L 3


RESULT   8
P92421
ID   P92421      PRELIMINARY;      PRT;     7 AA.
AC   P92421; P92419;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
DE   RIBOSOMAL PROTEIN 11 (FRAGMENT).
GN   RPS11.
OS   Psathyrostachys fragilis.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Psathyrostachys.
OX   NCBI_TaxID=37729;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H4372, AND H917; TISSUE=LEAVES;
RA   Petersen G., Seberg O.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77753; CAB01337.1; -.
DR   EMBL; Z77752; CAB01334.1; -.
KW   Ribosomal protein; Chloroplast.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  894 MW;  6734140333277700 CRC64;


  Query Match             36.4%;  Score 4;  DB 8;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 L 7


RESULT   9
P92385
ID   P92385      PRELIMINARY;      PRT;     7 AA.
AC   P92385; P92383;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
DE   RIBOSOMAL PROTEIN 11 (FRAGMENT).
GN   RPS11.
OS   Hordeum marinum (Seaside barley).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4519;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H299, AND H801; TISSUE=LEAVES;
RA   Petersen G., Seberg O.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77763; CAB01367.1; -.
DR   EMBL; Z77762; CAB01364.1; -.
KW   Ribosomal protein; Chloroplast.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  894 MW;  6734140333277700 CRC64;


  Query Match             36.4%;  Score 4;  DB 8;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 L 7
```

```
RESULT  10
P92210
ID   P92210      PRELIMINARY;      PRT;     7 AA.
AC   P92210;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   RIBOSOMAL PROTEIN 11 (FRAGMENT).
GN   RPS11.
OS   Agropyron cristatum.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Agropyron.
OX   NCBI_TaxID=4593;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H4349; TISSUE=LEAVES;
RA   Petersen G., Seberg O.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77771; CAB01391.1; -.
KW   Ribosomal protein; Chloroplast.
FT   NON_TER       1       1
SQ   SEQUENCE   7 AA;  894 MW;  6734140333277700 CRC64;

  Query Match           36.4%;  Score 4;  DB 8;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 L 7


RESULT  11
P92214
ID   P92214      PRELIMINARY;      PRT;     7 AA.
AC   P92214;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   RIBOSOMAL PROTEIN 11 (FRAGMENT).
GN   RPS11.
OS   Amblyopyrum muticum.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Amblyopyrum.
OX   NCBI_TaxID=4595;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H5572; TISSUE=LEAVES;
RA   Petersen G., Seberg O.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77756; CAB01346.1; -.
KW   Ribosomal protein; Chloroplast.
FT   NON_TER       1       1
SQ   SEQUENCE   7 AA;  894 MW;  6734140333277700 CRC64;

  Query Match           36.4%;  Score 4;  DB 8;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 L 7


RESULT  12
P92218
ID   P92218      PRELIMINARY;      PRT;     7 AA.
AC   P92218;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   RIBOSOMAL PROTEIN 11 (FRAGMENT).
GN   RPS11.
OS   Australopyrum retrofractum.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Australopyrum.
OX   NCBI_TaxID=4597;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H6723; TISSUE=LEAVES;
RA   Petersen G., Seberg O.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77767; CAB01379.1; -.
KW   Ribosomal protein; Chloroplast.
FT   NON_TER       1       1
SQ   SEQUENCE   7 AA;  894 MW;  6734140333277700 CRC64;

  Query Match           36.4%;  Score 4;  DB 8;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 L 7


RESULT  13
P92221
ID   P92221      PRELIMINARY;      PRT;     7 AA.
AC   P92221;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   RIBOSOMAL PROTEIN 11 (FRAGMENT).
GN   RPS11.
OS   Bromus inermis (Smooth brome grass).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Bromeae; Bromus.
OX   NCBI_TaxID=15371;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OSA414; TISSUE=LEAVES;
RA   Petersen G., Seberg O.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77759; CAB01355.1; -.
KW   Ribosomal protein; Chloroplast.
FT   NON_TER       1       1
SQ   SEQUENCE   7 AA;  894 MW;  6734140333277700 CRC64;

  Query Match           36.4%;  Score 4;  DB 8;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 L 7


RESULT  14
P92226
ID   P92226      PRELIMINARY;      PRT;     7 AA.
AC   P92226;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
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```
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   RIBOSOMAL PROTEIN 11 (FRAGMENT).
GN   RPS11.
OS   Crithopsis delileana.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Crithopsis.
OX   NCBI_TaxID=37674;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H5558; TISSUE=LEAVES;
RA   Petersen G., Seberg O.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77751; CAB01331.1; -.
KW   Ribosomal protein; Chloroplast.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  894 MW;  6734140333277700 CRC64;


  Query Match             36.4%;  Score 4;  DB 8;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 L 7


RESULT  15
P92372
ID   P92372      PRELIMINARY;      PRT;     7 AA.
AC   P92372;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   RIBOSOMAL PROTEIN 11 (FRAGMENT).
GN   RPS11.
OS   Haynaldia villosa.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC   Panicoideae; Andropogoneae; Haynaldia.
OX   NCBI_TaxID=40247;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H5561; TISSUE=LEAVES;
RA   Petersen G., Seberg O.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77741; CAB01301.1; -.
KW   Ribosomal protein; Chloroplast.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  894 MW;  6734140333277700 CRC64;


  Query Match             36.4%;  Score 4;  DB 8;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 L 7


Search completed: December 13, 2001, 10:50:31
Job time: 320 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:46:23 ; Search time 38.61 Seconds
(without alignments)
15.348 Million cell updates/sec

Title: US-09-424-080A-2
Perfect score: 11
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	36.4	2	21	AAB44925	Human secreted pro
2	4	36.4	2	21	AAB27827	Human secreted pro
3	4	36.4	2	22	AAG99717	ERA binding domain
4	4	36.4	2	22	AAB91562	Endothelins and re
5	4	36.4	2	22	AAB91740	Opioid peptide SEQ
6	4	36.4	2	22	AAB91749	Opioid peptide SEQ
7	4	36.4	3	10	AAP93533	N-terminal portion
8	4	36.4	3	10	AAP93348	Portion of myc var
9	4	36.4	3	10	AAP90667	New antihypertensi
10	4	36.4	3	11	AAR07037	Low toxicity immun
11	4	36.4	3	11	AAR07580	Hypotensive polype
12	4	36.4	3	12	AAR10543	Hypotensive oligop
13	4	36.4	3	14	AAR38486	Human RDS Pro216Le
14	4	36.4	3	14	AAR39998	Scintigraph imagin
15	4	36.4	3	14	AAR59412	Angiotensin conver
16	4	36.4	3	15	AAR65950	Tripeptide inhibit
17	4	36.4	3	15	AAR46817	Phytase derived pe
18	4	36.4	3	15	AAR48960	NL4-3 truncated GA
19	4	36.4	3	15	AAR49510	Endothelin antagon
20	4	36.4	3	15	AAR51439	IGF-1 analogue N-t
21	4	36.4	3	15	AAR51440	IGF-1 analogue N-t
22	4	36.4	3	15	AAR51441	IGF-1 analogue N-t
23	4	36.4	3	15	AAR58569	Angiotensin I conv
24	4	36.4	3	15	AAR58570	Angiotensin I conv
25	4	36.4	3	15	AAR58571	Angiotensin I conv
26	4	36.4	3	16	AAR75205	Microbial emetic t
27	4	36.4	3	16	AAR82733	Apolipoprotein A-I
28	4	36.4	3	16	AAR82737	Apolipoprotein A-I
29	4	36.4	3	16	AAR82740	Apolipoprotein A-I
30	4	36.4	3	16	AAR82744	Apolipoprotein A-I
31	4	36.4	3	16	AAR82919	Non-RGD, non-YISGR
32	4	36.4	3	16	AAR82907	Non-RGD, non-YISGR
33	4	36.4	3	16	AAR64432	DP-178 homologue 3
34	4	36.4	3	16	AAR64398	DP-178 homologue 1
35	4	36.4	3	16	AAR64689	HPF3 peptide deriv
36	4	36.4	3	16	AAR64624	HPF3 peptide deriv
37	4	36.4	3	17	AAR99823	Active domain from
38	4	36.4	3	17	AAR99825	Mutant chemokine a
39	4	36.4	3	17	AAR99826	Mutant chemokine a
40	4	36.4	3	17	AAR99827	Mutant chemokine a
41	4	36.4	3	17	AAR99828	Active domain from
42	4	36.4	3	17	AAR88898	Small synthetic an
43	4	36.4	3	18	AAW31319	Human Interleukin-
44	4	36.4	3	18	AAW31314	Human Interleukin-
45	4	36.4	3	21	AAY79636	Peroxisome reactan

ALIGNMENTS

RESULT 1
AAB44925
ID AAB44925 standard; Protein; 2 AA.
XX
AC AAB44925;
XX
DT 12-FEB-2001 (first entry)
XX
DE Human secreted protein encoded by gene 9.
XX
KW Secreted protein; human; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW nootropic; neuroprotective; antibacterial; virucide; fungicide;
KW ophthalmological; gene therapy; treatment; autoimmune disease; infection;
KW cardiovascular disorder; nervous system disorder; ocular disorder;
KW wound healing; epithelial cell proliferation; skin aging; mental state;
KW transplantation; metabolism modulation.
XX
OS Homo sapiens.
XX
PN WO200055200-A1.
XX
PD 21-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US06042.
XX
PR 12-MAR-1999; 99US-0124143.
PR 03-DEC-1999; 99US-0168663.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-656008/63.

```
DR   N-PSDB; AAC79906.
XX
PT   Isolated human secretory proteins, nucleic acids encoding them and
PT   antibodies directed against them, useful for diagnosing and treating
PT   disorders related to the proteins such as cancer, Alzheimer's disease
PT   and Parkinsons -
XX
PS   Claim 11; Page 383; 453pp; English.
XX
CC   This invention describes a novel isolated polypeptide (I) and its
CC   encoding nucleic acid molecule (II) which have immunosuppressive,
CC   antiarthritic, antirheumatic, antiproliferative, cytostatic, cardiant,
CC   vasotropic, cerebroprotective, nootropic, neuroprotective, antibacterial,
CC   virucide, fungicide and ophthalmological activity and which can be used
CC   for gene therapy. (I) and (II) are used to prevent, treat or ameliorate
CC   a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
CC   dogs, chickens or sheep. (I) and (II) are also used in diagnosing a
CC   pathological condition or susceptibility to a pathological condition. The
CC   antibodies to (II) can also be used in alleviating symptoms associated
CC   with the disorders and in diagnostic immunoassays e.g. radioimmunoassays
CC   or enzyme linked immunosorbent assays (ELISA). Disorders which are
CC   diagnosed or treated include autoimmune diseases e.g. rheumatoid
CC   arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC   liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC   disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC   e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC   fungi and ocular disorders e.g. corneal infection. The polypeptides can
CC   also be used to aid wound healing and epithelial cell proliferation, to
CC   prevent skin aging due to sunburn, to maintain organs before
CC   transplantation, for supporting cell culture of primary tissues, to
CC   regenerate tissues and in chemotaxis. The polypeptides are used to
CC   modulate mammalian metabolism, to change mammal's mental state or
CC   physical state by influencing biorhythms circadian rhythms, depression
CC   tendency for violence tolerance for pain, reproductive capabilities,
CC   hormonal or endocrine levels, appetite, libido, memory, stress or other
CC   cognitive qualities, as a food additive or preservative, such as to
CC   increase or decrease storage capabilities, fat content, lipid, protein,
CC   carbohydrates, vitamins, minerals, cofactors or other nutritional
CC   components.
XX
SQ   Sequence   2 AA;

  Query Match             36.4%;  Score 4;  DB 21;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 1 1


RESULT   2
AAB27827
ID   AAB27827 standard; Protein; 2 AA.
XX
AC   AAB27827;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human secreted protein #34.
XX
KW   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW   antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW   vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW   cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; human; secreted protein.
XX
OS   Homo sapiens.
XX
PN   WO200055199-A1.
XX
PD   21-SEP-2000.
XX
PF   09-MAR-2000; 2000WO-US06014.
XX
PR   12-MAR-1999;   99US-0124095.
PR   11-JUN-1999;   99US-0138598.
PR   03-DEC-1999;   99US-0168665.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM,  Komatsoulis G;
XX
DR   WPI; 2000-572359/53.
DR   N-PSDB; AAC59248.
XX
PT   Isolated nucleic acid molecule encoding a human secreted protein is
PT   used in preventing, treating or ameliorating a medical condition  -
XX
PS   Claim 11; Page 385; 433pp; English.
XX
CC   Sequences AAB27794-B27840 represent the amino acid sequences of 47
CC   human secreted proteins encoded by the genes AAC59215-C59261. The genes
CC   and proteins are useful for preventing, ameliorating or treating medical
CC   conditions, e.g. by protein or gene therapy. The genes are isolated from
CC   a range of human tissues disclosed in the specification. The nucleic
CC   acids, proteins, antibodies and (ant)agonists are useful in the
CC   diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC   ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC   marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC   (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC   Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC   colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC   (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC   epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC   and parasitic infections.
XX
SQ   Sequence   2 AA;

  Query Match             36.4%;  Score 4;  DB 21;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 1 1


RESULT   3
AAG99717
ID   AAG99717 standard; Peptide; 2 AA.
XX
AC   AAG99717;
XX
DT   27-SEP-2001  (first entry)
XX
DE   ERA binding domain polypeptide SEQ ID NO 159.
XX
KW   ERA binding domain; Escherichia coli; GTPase; antimicrobial;
KW   antibacterial; antibiotic; pathogenesis; infection; vaccine;
KW   peptide therapy.
XX
OS   Streptococcus thermophilus.
XX
PN   WO200153458-A2.
XX
PD   26-JUL-2001.
XX
PF   17-JAN-2001; 2001WO-US01786.
XX
PR   18-JAN-2000; 2000US-0176870.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
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PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Lupas AN, Pearce KH;
XX
DR WPI; 2001-476108/51.
XX
PT New ERA binding domain polypeptides and polynucleotides encoding them,
PT useful as research reagents and materials for discovery of treatments
PT and diagnostics for diseases, or for genetic immunisation -
XX
PS Claim 1; Page 26; 279pp; English.
XX
CC The present invention relates to ERA binding domain polypeptides
CC (AAG99559-AAG99989 and AAM00010-AAM00021). The era gene in Escherichia
CC coli codes for an essential GTPase protein able to autophosphorylate at
CC serine and/or threonine residues. The protein has potential antimicrobial
CC and antibacterial activity and is useful in screening for antagonists,
CC agonists and for compounds with antibiotic activity. The proteins are
CC also useful in determining their role in pathogenesis of infection,
CC dysfunction and disease and could be used as part of a vaccine and/or
CC peptide therapy.
XX
SQ Sequence 2 AA;

Query Match 36.4%; Score 4; DB 22; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 1 1 1

RESULT 4
AAB91562
ID AAB91562 standard; Peptide; 2 AA.
XX
AC AAB91562;
XX
DT 22-JUN-2001 (first entry)
XX
DE Endothelins and related peptides SEQ ID NO:738.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT -
XX
PS Disclosure; Page 438; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 2 AA;

Query Match 36.4%; Score 4; DB 22; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 1 1 1

RESULT 5
AAB91740
ID AAB91740 standard; Peptide; 2 AA.
XX
AC AAB91740;
XX
DT 22-JUN-2001 (first entry)
XX
DE Opioid peptide SEQ ID NO:916.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT -
XX
PS Disclosure; Page 492; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 2 AA;

Query Match 36.4%; Score 4; DB 22; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 1 l 1

RESULT 6
AAB91749
ID AAB91749 standard; Peptide; 2 AA.
XX
AC AAB91749;
XX
DT 22-JUN-2001 (first entry)
XX
DE Opioid peptide SEQ ID NO:925.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
PS Disclosure; Page 495; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 2 AA;

Query Match 36.4%; Score 4; DB 22; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 l 2

RESULT 7
AAP93533
ID AAP93533 standard; protein; 3 AA.
XX
AC AAP93533;
XX
DT 06-JUN-1990 (first entry)
XX
DE N-terminal portion of the leader peptide of the heavy chain variable
DE region (VH) gene as encoded in T15.
XX
KW Mammalian immunoglobulin; mammalian T-cell receptor;
KW chimeric polypeptide; TEPC 15VH; heavy chain variable region; T15 VH;
KW anti-tumour activity; MMuLV-LTR; MMuLV-LTR-VH.
XX
PN JP01063394-A.
XX
PD 09-MAR-1989.
XX
PF 04-SEP-1987; 87JP-0221758.
XX
PR 04-SEP-1987; 87JP-0221758.
XX
PA (FUJI-) FUJITA GAKUEN GH (KYOW).
XX
DR WPI; 1989-118256/16.
DR N-PSDB; AAN92384.
XX
PT New chimeric polypeptide having antitumour activity -
PT contains variable region of mammalian immunoglobulin and
PT constant region of mammalian T-cell receptor
XX
PS Disclosure; page 23 (2); 29pp; Japanese.
XX
CC The coding sequence for the H chain variable region (VH) in TEPC 15VH,
CC and MMuLV-LTR were subcloned in order to prepare MMuLV-LTR-VH, as part of
CC the process of preparing a new chimeric polypeptide containing the
CC variable region of mammalian immunoglobulin and the constant region of
CC mammalian T-cell receptor. The chimeric polypeptide is expected to confer
CC anti-tumour activity on cells.
XX
SQ Sequence 3 AA;

Query Match 36.4%; Score 4; DB 10; Length 3;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 3 l 3

```
RESULT   8
AAP93348
ID   AAP93348 standard; protein; 3 AA.
XX
AC   AAP93348;
XX
DT   24-JUN-1990  (first entry)
XX
DE   Portion of myc variant as encoded by pMYC-A.
XX
KW   C-myc; variant myc protein; pMYC-A.
XX
PN   JP01039999-A.
XX
PD   10-FEB-1989.
XX
PF   06-AUG-1987;   87JP-0197197.
XX
PR   06-AUG-1987;   87JP-0197197.
XX
PA   (MITK ) MITSUI TOATSU CHEM INC.
XX
DR   WPI; 1989-089714/12.
DR   N-PSDB; AAN91367.
XX
PT   Myc protein for antibody prepn. -
PT   is stabilised by converting aminoacid(s) of myc protein to other
PT   aminoacid to produce variant type myc protein
XX
PS   Fig 3.4.; page 17; 18pp; Japanese.
XX
CC   It is a variant of C-myc protein. In the patent, myc protein in the host
CC   cell is stabilised by converting at least one amino acid to another amino
CC   acid, while not affecting the properties of the myc protein. The residue
CC   changed is the second one.
XX
SQ   Sequence   3 AA;


  Query Match             36.4%;  Score 4;  DB 10;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       3 1 3


RESULT   9
AAP90667
ID   AAP90667 standard; protein; 3 AA.
XX
AC   AAP90667;
XX
DT   26-MAY-1990  (first entry)
XX
DE   New antihypertensive peptide.
XX
KW   Antihypertensive peptide; angiotensin-converting enzyme;
KW   ACE.
XX
PN   JP01083096-A.
XX
PD   28-MAR-1989.
XX
PF   25-SEP-1987;   87JP-0241646.
XX
PR   25-SEP-1987;   87JP-0241646.
XX
PA   (AJIN ) AJINOMOTO KK.
XX
DR   WPI; 1989-136272/18.
XX
PT   New antihypertensive peptide(s) -
PT   used to inhibit angiotensin-converting enzyme
XX
PS   ; ; 20pp; Japanese.
XX
CC   The peptide and its salts inhibit angiotensin-converting
CC   enzyme (ACE) and are useful as antihypertensives. They may be
CC   administered orally, parenterally or rectally in the form of tablets,
CC   capsules, granules, powder, syrup, suspension, suppositories,
CC   ointment, cream, gel, plaster, inhalation compsn. or
CC   injection at a dose of 0.001-1000, pref. 0.01-10, mg, 1-3 times per day.
XX
SQ   Sequence   3 AA;


  Query Match             36.4%;  Score 4;  DB 10;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       1 1 1


RESULT   10
AAR07037
ID   AAR07037 standard; protein; 3 AA.
XX
AC   AAR07037;
XX
DT   23-NOV-1990  (first entry)
XX
DE   Low toxicity immunosuppressant short peptide.
XX
KW   Immunosuppressant; T-lymphocyte; macrophage.
XX
OS   Synthetic.
XX
PN   EP378432-A.
XX
PD   18-JUL-1990.
XX
PF   12-JAN-1990;   90EP-0300355.
XX
PR   13-JAN-1989;   89HU-0000116.
XX
PA   (RICT ) RICHTER GEDEON VEGY.
XX
PI   SCHON I,  NYEKI O,  KISFALUDY L,  LASZLO D,  HAJOS G,  SZPORNY L;
XX
DR   WPI; 1990-218773/29.
XX
PT   New low toxicity immunosuppressive short peptide(s) - which
PT   inhibit maturation of T-lymphocytes and activity of macrophage(s).
XX
PS   Claim 1; Page 14; 15pp; English.
XX
CC   Peptides inhibit T-lymphocyte maturation and macrophage activity.
CC   Immunosuppressants decompose rapidly and have low toxicity.
XX
SQ   Sequence   3 AA;


  Query Match             36.4%;  Score 4;  DB 11;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       3 1 3
```

```
RESULT  11
AAR07580
ID   AAR07580 standard; peptide; 3 AA.
XX
AC   AAR07580;
XX
DT   08-FEB-1991  (first entry)
XX
DE   Hypotensive polypeptide.
XX
KW   Gamma-casein.
XX
OS   Zea mays.
XX
PN   JP02240027-A.
XX
PD   25-SEP-1990.
XX
PF   14-MAR-1989;   89JP-0059549.
XX
PR   14-MAR-1989;   89JP-0059549.
XX
PA   (AGEN ) AGENCY OF IND SCI TECH.
PA   (SHOS ) SHOWA KK.
XX
DR   WPI; 1990-332335/44.
XX
PT   New polypeptide hypotensive agents - are tri-, penta- or
PT   hexa:peptide(s) derived from gamma casein
XX
PS   Claim 1; Page 193; 5pp; Japanese.
XX
CC   Peptide, derived from Zea mays gamma-casein, is useful as an anti-
CC   hypertensive agent in mammals and humans.
XX
SQ   Sequence   3 AA;

  Query Match             36.4%;  Score 4;  DB 11;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 1 1


RESULT  12
AAR10543
ID   AAR10543 standard; Protein; 3 AA.
XX
AC   AAR10543;
XX
DT   15-MAR-1991  (first entry)
XX
DE   Hypotensive oligopeptide.
XX
KW   Oral hypotensive; fig.
XX
OS   Ficus carica.
XX
PN   JP02282394-A.
XX
PD   19-NOV-1990.
XX
PF   24-APR-1989;   89JP-0104265.
XX
PR   24-APR-1989;   89JP-0104265.
XX
PA   (AGEN ) AGENCY OF IND SCI TECH.
PA   (SHOS ) SHOWA SANGYO KK.
XX
DR   WPI; 1991-004480/01.
XX
PT   New oligopeptide hypotensive drug - based on alanine, valine,
PT   asparagine, proline, isoleucine and arginine
XX
PS   Claim 1; Page 843; 9pp; Japanese.
XX
CC   Peptides may be derived from extract of fig, and are hypotensive
CC   agents.
XX
SQ   Sequence   3 AA;

  Query Match             36.4%;  Score 4;  DB 12;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 1 1


RESULT  13
AAR38486
ID   AAR38486 standard; Protein; 3 AA.
XX
AC   AAR38486;
XX
DT   11-NOV-1993  (first entry)
XX
DE   Human RDS Pro216Leu fragment.
XX
KW   Human; mutant; retinal degeneration; primer; rds; RDS; photoreceptor;
KW   hereditary; retinitis pigmentosa; amplify; retina; murine; autosomal;
KW   dominant; PCR.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2
FT                   /note= "Pro216Leu"
XX
PN   WO9312134-A.
XX
PD   24-JUN-1993.
XX
PF   08-DEC-1992;   92WO-US10536.
XX
PR   11-DEC-1991;   91US-0805123.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Berson EL,  Dryja TP;
XX
DR   WPI; 1993-214088/26.
DR   N-PSDB; AAQ43555.
XX
PT   Probe or primer contg. sequence of human retinal degeneration
PT   slow protein mutant - used to diagnose hereditary retinal
PT   degenerative diseases
XX
PS   Disclosure; Fig 13B; 56pp; English.
XX
CC   The sequences given in AAR38485-87 represent regions of the human
CC   retinal degenaration slow (RDS) protein which contain mutations.
CC   These mutations of the human RDS protein cosegregate with autosomal
CC   dominant retinitis pigmentosa.  The RDS gene sequence was isolated
CC   via the murine rds gene and has been mapped to chromosome 6p.  The
CC   murine rds gene is a semidominant mutation with a phenotype of
CC   abnormal development of rod and cone photoreceptors, followed by
CC   their slow degeneration.  The DNA encoding the mutation containing
CC   regions was isolated by polymerase chain reaction (PCR) using primers
CC   derived from RDS gene intron flanking sequences.
```

```
XX
SQ   Sequence   3 AA;


  Query Match             36.4%;  Score 4;  DB 14;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 l 2


RESULT  14
AAR39998
ID   AAR39998 standard; peptide; 3 AA.
XX
AC   AAR39998;
XX
DT   23-MAY-1994  (first entry)
XX
DE   Scintigraph imaging agent specific binding peptide.
XX
KW   Reagent; site imaging; technetium-99M labelled; peptide.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "formyl-Met"
XX
PN   WO9321962-A.
XX
PD   11-NOV-1993.
XX
PF   19-APR-1993;   93WO-US03687.
XX
PR   30-APR-1992;   92US-0871282.
XX
PA   (DIAT-) DIATECH INC.
XX
PI   Buttram S,  Civitello ER,  Dean RT,  Lister-James J,  McBride W;
XX
DR   WPI; 1993-368429/46.
XX
PT   Reagents for preparing scintigraphic imaging agents - contg.
PT   technetium-99M labelled peptide(s) contg. 3-100 aminoacid(s)
XX
PS   Claim 35; Page 39; 55pp; English.
XX
CC   The sequence is that of a specific binding peptide used as part of
CC   a reagent for preparing a scintigraphic imaging agent for imaging
CC   sites within a mammalian body. In this the peptide is covalently
CC   linked to a radiolabel-binding moiety which is capable of forming
CC   a complex with a radioisotope, pref. technetium-99M.
XX
SQ   Sequence   3 AA;


  Query Match             36.4%;  Score 4;  DB 14;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 l 2


RESULT  15
AAR59412
ID   AAR59412 standard; peptide; 3 AA.
XX
AC   AAR59412;
XX
DT   08-NOV-1994  (first entry)
XX
DE   Angiotensin converting enzyme inhibitor.
XX
KW   Angiotensin converting enzyme inhibitor; ACE; antihypertensive;
KW   hypertension.
XX
OS   Clupea pilchardus.
XX
PN   JP05262790-A.
XX
PD   12-OCT-1993.
XX
PF   03-JUN-1991;   91JP-0157355.
XX
PR   03-JUN-1991;   91JP-0157355.
XX
PA   (SENM-) SENMI EKISU KK.
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1993-357193/45.
XX
PT   New angiotensin I converting enzyme inhibiting peptide(s) - used
PT   for treating hypertension and in foods
XX
PS   Claim 1; Page 2; 6pp; Japanese.
XX
CC   The peptide is an angiotensin converting enzyme inhibitor which may
CC   be used for treating hypertension or in foods. It is obtained by
CC   hydrolysis of actin-containing protein, e.g. sardine paste.
XX
SQ   Sequence   3 AA;


  Query Match             36.4%;  Score 4;  DB 14;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 l 1


Search completed: December 13, 2001, 10:46:24
Job time: 104 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 10:45:08 ; Search time 19.94 Seconds
(without alignments)
9.028 Million cell updates/sec

Title: US-09-424-080A-2
Perfect score: 11
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	36.4	2	2	US-08-451-822A-19	Sequence 19, Appl
2	4	36.4	2	2	US-08-915-414A-6	Sequence 6, Appli
3	4	36.4	2	3	US-09-039-308A-4	Sequence 4, Appli
4	4	36.4	3	1	US-07-663-413-7	Sequence 7, Appli
5	4	36.4	3	1	US-07-663-413-10	Sequence 10, Appl
6	4	36.4	3	1	US-07-840-077A-3	Sequence 3, Appli
7	4	36.4	3	1	US-07-947-035-3	Sequence 3, Appli
8	4	36.4	3	1	US-07-947-035-4	Sequence 4, Appli
9	4	36.4	3	1	US-07-947-035-5	Sequence 5, Appli
10	4	36.4	3	1	US-08-055-530-7	Sequence 7, Appli
11	4	36.4	3	1	US-08-055-530-10	Sequence 10, Appl
12	4	36.4	3	1	US-08-082-853-2	Sequence 2, Appli
13	4	36.4	3	1	US-08-081-539-117	Sequence 117, App
14	4	36.4	3	1	US-08-221-582A-2	Sequence 2, Appli
15	4	36.4	3	1	US-08-167-336A-3	Sequence 3, Appli
16	4	36.4	3	1	US-08-466-647-117	Sequence 117, App
17	4	36.4	3	1	US-08-288-681A-6	Sequence 6, Appli
18	4	36.4	3	1	US-08-305-768-26	Sequence 26, Appl
19	4	36.4	3	1	US-08-411-389-20	Sequence 20, Appl
20	4	36.4	3	1	US-08-213-897A-9	Sequence 9, Appli
21	4	36.4	3	1	US-08-213-897A-10	Sequence 10, Appl
22	4	36.4	3	1	US-08-179-481-116	Sequence 116, App
23	4	36.4	3	1	US-08-179-984-2	Sequence 2, Appli
24	4	36.4	3	1	US-08-416-962-3	Sequence 3, Appli
25	4	36.4	3	1	US-08-321-585A-1	Sequence 1, Appli
26	4	36.4	3	1	US-08-321-585A-2	Sequence 2, Appli
27	4	36.4	3	1	US-08-321-585A-3	Sequence 3, Appli
28	4	36.4	3	1	US-08-464-456-25	Sequence 25, Appl
29	4	36.4	3	1	US-08-454-950-3	Sequence 3, Appli
30	4	36.4	3	1	US-08-634-060-36	Sequence 36, Appl
31	4	36.4	3	1	US-08-338-282-11	Sequence 11, Appl
32	4	36.4	3	1	US-08-741-678-6	Sequence 6, Appli
33	4	36.4	3	1	US-08-406-192-45	Sequence 45, Appl
34	4	36.4	3	1	US-08-589-011-3	Sequence 3, Appli
35	4	36.4	3	1	US-08-269-929-2	Sequence 2, Appli
36	4	36.4	3	1	US-08-454-949-3	Sequence 3, Appli
37	4	36.4	3	1	US-08-153-848-17	Sequence 17, Appl
38	4	36.4	3	1	US-08-443-675-2	Sequence 2, Appli
39	4	36.4	3	1	US-08-447-010-17	Sequence 17, Appl
40	4	36.4	3	1	US-08-445-206-2	Sequence 2, Appli
41	4	36.4	3	1	US-07-923-724-44	Sequence 44, Appl
42	4	36.4	3	1	US-08-843-035-30	Sequence 30, Appl
43	4	36.4	3	1	US-08-463-052-25	Sequence 25, Appl
44	4	36.4	3	1	US-08-470-837-7	Sequence 7, Appli
45	4	36.4	3	4	US-09-383-630-9	Sequence 9, Appli

ALIGNMENTS

```
RESULT   1
US-08-451-822A-19
; Sequence 19, Application US/08451822A
; Patent No. 5863888
;  GENERAL INFORMATION:
;    APPLICANT:  Dionne, Craig A
;    APPLICANT:  Crumley, Greg
;    APPLICANT:  Jaye, Michael C
;    APPLICANT:  Schlessinger, Joseph
;    TITLE OF INVENTION:  Fibroblast Growth Factor Receptors
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Legal Department
;      STREET:  500 Arcola Road
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/451,822A
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/323,430
;      FILING DATE:  14-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/934,372
;      FILING DATE:  21-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/549,587
;      FILING DATE:  06-JUL-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Savitzky, Martin
;      REGISTRATION NUMBER:  29,699
;      REFERENCE/DOCKET NUMBER:  A0496E
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-3816
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
```

```
US-08-451-822A-19


  Query Match             36.4%;  Score 4;  DB 2;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 L 2


RESULT   2
US-08-915-414A-6
; Sequence 6, Application US/08915414A
; Patent No. 5976822
;  GENERAL INFORMATION:
;    APPLICANT:  LANDRUM, ET AL.
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR MONITORING APOPTOSIS
;    TITLE OF INVENTION:  AND DISTINGUISHING APOPTOSIS FROM NECROSIS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MITCHELL ALTER, COULTER INTERN. CORP.
;      STREET:  11800 SW 147 AVE.
;      CITY:  MIAMI
;      STATE:  FLORIDA
;      COUNTRY:  USA
;      ZIP:  33196
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MB storage
;      COMPUTER:  IBM PC
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Microsoft Word 6.0/95
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/915,414A
;      FILING DATE:  20-AUG-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/444,051
;      FILING DATE:  18-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MITCHELL E. ALTER
;      REGISTRATION NUMBER:  28,684
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (305) 380-3636
;      TELEFAX:  (305) 380-4566
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-915-414A-6


  Query Match             36.4%;  Score 4;  DB 2;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT   3
US-09-039-308A-4
; Sequence 4, Application US/09039308A
; Patent No. 6069129
;  GENERAL INFORMATION:
;    APPLICANT:  Sandberg, Lawrence; Roos, Phillip;
;    APPLICANT:  Mitts, Thomas
;    TITLE OF INVENTION:  ELASTIN DERIVED COMPOSITION
;    TITLE OF INVENTION:  AND METHOD OF
;    TITLE OF INVENTION:  USING SAME
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  REED SMITH SHAW & MCCLAY, LLP
;      STREET:  PO Box 488
;      CITY:  Pittsburgh
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  15230
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  Compaq
;      OPERATING SYSTEM:  Microsoft Windows 95
;      SOFTWARE:  Word 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/039,308A
;      FILING DATE:  March 13, 1998
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Miller, Raymond A.
;      REGISTRATION NUMBER:  42,891
;      REFERENCE/DOCKET NUMBER:  97-489
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (412) 288-4192
;      TELEFAX:  (412) 288-3300
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-039-308A-4


  Query Match             36.4%;  Score 4;  DB 3;  Length 2;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT   4
US-07-663-413-7
; Sequence 7, Application US/07663413
; Patent No. 5240703
;  GENERAL INFORMATION:
;    APPLICANT:  Cochran, Mark D.
;    TITLE OF INVENTION:  ATTENUATED, GENETICALLY-ENGINEERED
;    TITLE OF INVENTION:  PSEUDORABIES VIRUS S-PRV-155 AND USESTHEREOF
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John P. White, Esq.
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/663,413
;      FILING DATE:  19910301
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White Esq., John P.
;      REGISTRATION NUMBER:  28,678
```

; REFERENCE/DOCKET NUMBER: 38720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-663-413-7

Query Match 36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 5
US-07-663-413-10
; Sequence 10, Application US/07663413
; Patent No. 5240703
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED
; TITLE OF INVENTION: PSEUDORABIES VIRUS S-PRV-155 AND USESTHEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/663,413
; FILING DATE: 19910301
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-663-413-10

Query Match 36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 6
US-07-840-077A-3
; Sequence 3, Application US/07840077A
; Patent No. 5443816
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT: Zamora, Paul O.
; APPLICANT: Rhodes, Buck A.
; TITLE OF INVENTION: Peptide-Metal Ion
; TITLE OF INVENTION: Pharmaceutical Preparation and Method
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RhoMed Incorporated
; STREET: 4261 Balloon Park
; CITY: Albuquerque
; STATE: NM
; COUNTRY: U.S.A.
; ZIP: 87109-5802
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM PC/XT/AT, IBM PS/2 or
; COMPUTER: compatibles
; OPERATING SYSTEM: PC-DOS or MS-DOS
; SOFTWARE: WordPerfect 6.0a for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/840,077A
; FILING DATE: 20-FEB-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/816,477
; FILING DATE: 03-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Deborah A. Peacock
; REGISTRATION NUMBER: 31,649
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (505) 242-9677
; TELEFAX: (505) 243-2542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: No
; ANTI-SENSE: No
US-07-840-077A-3

Query Match 36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 7
US-07-947-035-3
; Sequence 3, Application US/07947035
; Patent No. 5444045
; GENERAL INFORMATION:
; APPLICANT: Francis, Geoffrey L.
; APPLICANT: Walton, Paul E.
; APPLICANT: Ballard, Francis J.
; APPLICANT: McMurty, John P.
; APPLICANT: Phelps, Patricia V.
; TITLE OF INVENTION: Method of Administering IGF-1, IGF-2,
; TITLE OF INVENTION: and Analogs Thereof to Birds
; NUMBER OF SEQUENCES: 18

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenneth D. Sibley
;      STREET:  P.O. Drawer 34009
;      CITY:  Charlotte
;      STATE:  No. 5444045th Carolina
;      COUNTRY:  US
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/947,035
;      FILING DATE:  17-SEP-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5175-59
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 881-3140
;      TELEFAX:  (919) 881-3175
;      TELEX:  575102
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
US-07-947-035-3


  Query Match             36.4%;  Score 4;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 L 2


RESULT   8
US-07-947-035-4
; Sequence 4, Application US/07947035
; Patent No. 5444045
;  GENERAL INFORMATION:
;    APPLICANT:  Francis, Geoffrey L.
;    APPLICANT:  Walton, Paul E.
;    APPLICANT:  Ballard, Francis J.
;    APPLICANT:  McMurty, John P.
;    APPLICANT:  Phelps, Patricia V.
;    TITLE OF INVENTION:  Method of Administering IGF-1, IGF-2,
;    TITLE OF INVENTION:  and Analogs Thereof to Birds
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenneth D. Sibley
;      STREET:  P.O. Drawer 34009
;      CITY:  Charlotte
;      STATE:  No. 5444045th Carolina
;      COUNTRY:  US
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/947,035
;      FILING DATE:  17-SEP-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5175-59
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 881-3140
;      TELEFAX:  (919) 881-3175
;      TELEX:  575102
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
US-07-947-035-4


  Query Match             36.4%;  Score 4;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 L 2


RESULT   9
US-07-947-035-5
; Sequence 5, Application US/07947035
; Patent No. 5444045
;  GENERAL INFORMATION:
;    APPLICANT:  Francis, Geoffrey L.
;    APPLICANT:  Walton, Paul E.
;    APPLICANT:  Ballard, Francis J.
;    APPLICANT:  McMurty, John P.
;    APPLICANT:  Phelps, Patricia V.
;    TITLE OF INVENTION:  Method of Administering IGF-1, IGF-2,
;    TITLE OF INVENTION:  and Analogs Thereof to Birds
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenneth D. Sibley
;      STREET:  P.O. Drawer 34009
;      CITY:  Charlotte
;      STATE:  No. 5444045th Carolina
;      COUNTRY:  US
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/947,035
;      FILING DATE:  17-SEP-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5175-59
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 881-3140
;      TELEFAX:  (919) 881-3175
;      TELEX:  575102
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
```

US-07-947-035-5

Query Match 36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 10
US-08-055-530-7
; Sequence 7, Application US/08055530
; Patent No. 5451499
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED
; TITLE OF INVENTION: PSEUDORABIES VIRUS S-PRV-155 AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/055,530
; FILING DATE: 19930430
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38720-Z/JPW/JEL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-055-530-7

Query Match 36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 11
US-08-055-530-10
; Sequence 10, Application US/08055530
; Patent No. 5451499
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED
; TITLE OF INVENTION: PSEUDORABIES VIRUS S-PRV-155 AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/055,530
; FILING DATE: 19930430
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38720-Z/JPW/JEL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-055-530-10

Query Match 36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 12
US-08-082-853-2
; Sequence 2, Application US/08082853
; Patent No. 5496718
; GENERAL INFORMATION:
; APPLICANT: HASHIMOTO, NOBUKAZU
; APPLICANT: MOCHIZUKI, HIDEO
; APPLICANT: HAMAI, AKIO
; APPLICANT: ISHIKAWA, SHINICHI
; APPLICANT: TORIKAI, MISAKO
; APPLICANT: MIYACHI, ISAO
; TITLE OF INVENTION: CHONDROITINASE, PROCESS FOR PREPARING
; TITLE OF INVENTION: THE SAME, AND PHARMACEUTICAL COMPOSITION COMPRISING THE
; TITLE OF INVENTION: SAME.
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,853
; FILING DATE: 19930623

```
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  CAMPBELL ESQ, PAULA A.
;       REGISTRATION NUMBER:  32,503
;       REFERENCE/DOCKET NUMBER:  3999/1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-248-7263
;       TELEFAX:  617-248-7100
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FEATURE:
;       NAME/KEY:  Protein
;       LOCATION:  1..3
;       OTHER INFORMATION:  /note= "C-terminal sequence of
;       OTHER INFORMATION:  Chondroitinase ABC"
US-08-082-853-2


  Query Match             36.4%;  Score 4;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       2 L 2


RESULT  13
US-08-081-539-117
; Sequence 117, Application US/08081539
; Patent No. 5501962
;  GENERAL INFORMATION:
;    APPLICANT:  Braford-Goldberg, Sarah R.
;    APPLICANT:  Easton, Alan M.
;    APPLICANT:  Klein, Barbara K.
;    APPLICANT:  McKearn, John P.
;    APPLICANT:  Olins, Peter O.
;    TITLE OF INVENTION:  Interleukin-3 (IL-3) Human/Murine
;    TITLE OF INVENTION:  Chimeric Hybrid Polypeptides
;    NUMBER OF SEQUENCES:  121
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mary Jo Kanady, G. D. Searle & Co., Corporate
;      ADDRESSEE:  Patent Dept.
;      STREET:  P. O. Box 5110
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60680
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/081,539
;      FILING DATE:  19930621
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kanady, Mary J.
;      REGISTRATION NUMBER:  28623
;      REFERENCE/DOCKET NUMBER:  2724
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (708)470-6501
;      TELEFAX:  (708)470-6881
;  INFORMATION FOR SEQ ID NO:  117:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-081-539-117


  Query Match             36.4%;  Score 4;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       2 L 2


RESULT  14
US-08-221-582A-2
; Sequence 2, Application US/08221582A
; Patent No. 5505946
;  GENERAL INFORMATION:
;    APPLICANT:  Ann R. Kennedy, Bernard F. Szuhaj
;    TITLE OF INVENTION:  Bowman-Birk Inhibitor Concentrate
;    TITLE OF INVENTION:  Compositions and Methods for the Treatment of Pre-Malignant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jane Massey Licata, Esq.
;      STREET:  210 Lake Drive East, Suite 201
;      CITY:  Cherry Hill
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM 486
;      OPERATING SYSTEM:  WINDOWS FOR WORKGROUPS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,582A
;      FILING DATE:  April 1, 1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/973,335
;      FILING DATE:  No. 5505946ember 2, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jane Massey Licata
;      REGISTRATION NUMBER:  32,257
;      REFERENCE/DOCKET NUMBER:  UPSC-0027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (609) 779-2400
;      TELEFAX:  (609) 779-8488
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-221-582A-2


  Query Match             36.4%;  Score 4;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       2 L 2


RESULT  15
US-08-167-336A-3
; Sequence 3, Application US/08167336A
; Patent No. 5531990
;  GENERAL INFORMATION:
;    APPLICANT:  THANAVALA, YASMIN
;    APPLICANT:  THAKUR, ARVIND
```

; APPLICANT: ROITT, IVAN
; APPLICANT: PRIDE, MICHAEL
; TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODY
; TITLE OF INVENTION: HAVING CORRESPONDENCE WITH HUMAN HEPATITIS
; TITLE OF INVENTION: B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DUNN & ASSOCIATES, P.C.
; STREET: P.O. BOX 96
; CITY: NEWFANE
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 14108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
; COMPUTER: VICTOR 300 SX/25
; OPERATING SYSTEM: MS-DOS VERSION 5.0
; SOFTWARE: WORDSTAR PROFESSIONAL RELEASE 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,336A
; FILING DATE: 15-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DUNN, MICHAEL L.
; REGISTRATION NUMBER: 25,330
; REFERENCE/DOCKET NUMBER: RPP:138 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 433-1661
; TELEFAX: (716) 433-1665
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3
; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE: PEPTIDE
; HYPOTHETICAL: NO
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-167-336A-3

Query Match 36.4%; Score 4; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

Search completed: December 13, 2001, 10:45:09
Job time: 29 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 12:01:34 ; Search time 12.48 Seconds
(without alignments)
23.503 Million cell updates/sec

Title: US-09-424-080A-2
Perfect score: 11
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 64

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	36.4	8	1	AKH_MELML	P25423 melolontha
2	4	36.4	8	1	AKH_TABAT	P14595 tabanus atr
3	4	36.4	8	1	AL12_CARMA	P81815 carcinus ma
4	4	36.4	8	1	AL15_CARMA	P81818 carcinus ma
5	4	36.4	8	1	AL16_CARMA	P81819 carcinus ma
6	4	36.4	8	1	AL17_CARMA	P81820 carcinus ma
7	4	36.4	8	1	AL18_CARMA	P81821 carcinus ma
8	4	36.4	8	1	ALL1_CYDPO	P82152 cydia pomon
9	4	36.4	8	1	ALL3_CYDPO	P82154 cydia pomon
10	4	36.4	8	1	ALL4_CALVO	P41840 calliphora
11	4	36.4	8	1	ALL4_CYDPO	P82155 cydia pomon
12	4	36.4	8	1	ALL5_CYDPO	P82156 cydia pomon
13	4	36.4	8	1	ALL6_CYDPO	P82157 cydia pomon
14	4	36.4	8	1	ALL7_CARMA	P81809 carcinus ma
15	4	36.4	8	1	ALL8_CARMA	P81811 carcinus ma
16	4	36.4	8	1	ALL9_CARMA	P81812 carcinus ma
17	4	36.4	8	1	CAD1_ENTFA	P13268 enterococcu
18	4	36.4	8	1	COXG_RAT	P80430 rattus norv
19	4	36.4	8	1	CPD1_ENTFA	P13269 enterococcu
20	4	36.4	8	1	FAR1_PANRE	P41872 panagrellus
21	4	36.4	8	1	FAR3_HOMAM	P41486 homarus ame
22	4	36.4	8	1	FAR4_HOMAM	P41487 homarus ame
23	4	36.4	8	1	HTF2_PERAM	P04549 periplaneta
24	4	36.4	8	1	HTF_TENMO	P25419 tenebrio mo
25	4	36.4	8	1	LMT2_LOCMI	P22396 locusta mig
26	4	36.4	8	1	LPK_LEUMA	P13049 leucophaea
27	4	36.4	8	1	LPMS_STAEP	P23211 staphylococ
28	4	36.4	8	1	NPB_BOVIN	P15507 bos taurus
29	4	36.4	8	1	PPK2_PERAM	P82692 periplaneta
30	4	36.4	8	1	RPCH_PANBO	P08939 pandalus bo
31	4	36.4	8	1	UPAA_HUMAN	P30096 homo sapien
32	2	18.2	8	1	ACI_THUAL	P18691 thunnus alb
33	2	18.2	8	1	ACT_CARMA	P80709 carcinus ma
34	2	18.2	8	1	ALL5_CALVO	P41841 calliphora
35	2	18.2	8	1	ANG2_BOTJA	Q10582 bothrops ja
36	2	18.2	8	1	B44K_PORGI	P81886 porphyromon
37	2	18.2	8	1	CCKN_MACEU	P30369 macropus eu
38	2	18.2	8	1	FAR7_ASCSU	P43171 ascaris suu
39	2	18.2	8	1	FAR8_CALVO	P41863 calliphora
40	2	18.2	8	1	FUSS_FUSSO	P81010 fusarium so
41	2	18.2	8	1	PLP_BRANA	P81707 brassica na
42	2	18.2	8	1	RS10_SALTY	O68928 salmonella
43	2	18.2	8	1	VGLG_HSV2B	P81780 herpes simp
44	1	9.1	8	1	AKHG_GRYBI	P14086 gryllus bim
45	1	9.1	8	1	AKH_LIBAU	P25418 libellula a

ALIGNMENTS

RESULT 1
AKH_MELML
ID AKH_MELML STANDARD; PRT; 8 AA.
AC P25423;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH).
OS Melolontha melolontha (Cockchafer),
OS Geotrupes stercorosus (Dor beetle), and
OS Pachnoda marginata (Flower beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
OX NCBI_TaxID=7061, 7087, 7058;
RN [1]
RP SEQUENCE.
RC SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
RX MEDLINE=91248100; PubMed=2039445;
RA Gaede G.;
RT "A unique charged tyrosine-containing member of the adipokinetic
RT hormone/red-pigment-concentrating hormone peptide family isolated and
RT sequenced from two beetle species.";
RL Biochem. J. 275:671-677(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;
RX MEDLINE=92265187; PubMed=1586453;
RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
RT "Primary structures of neuropeptides isolated from the corpora
RT cardiaca of various cetonid beetle species determined by
RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass
RT spectrometry.";
RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; S15422; S15422.
DR PIR; S21663; S21663.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;

Query Match 36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
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Db 2 L 2

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RESULT   2
AKH_TABAT
ID   AKH_TABAT      STANDARD;      PRT;     8 AA.
AC   P14595;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   ADIPOKINETIC HORMONE (AKH) (DIPTERAN CORPORA CARDIACA FACTOR I)
DE   (DCC I).
OS   Tabanus atratus (Horse fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
OC   Tabanidae; Tabanus.
OX   NCBI_TaxID=7207;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=90046758; PubMed=2813385;
RA   Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA   Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT   "Primary structure of two neuropeptide hormones with adipokinetic and
RT   hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT   flies (Diptera).";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC   -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC       CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC       DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC       MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; A33995; A33995.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Flight.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  949 MW;  86786771A9D1A736 CRC64;

  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      2 L 2


RESULT   3
AL12_CARMA
ID   AL12_CARMA     STANDARD;      PRT;     8 AA.
AC   P81815;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 12.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Multigene family.
SQ   SEQUENCE   8 AA;  913 MW;  672879CDCB569AB7 CRC64;

  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      8 L 8


RESULT   4
AL15_CARMA
ID   AL15_CARMA     STANDARD;      PRT;     8 AA.
AC   P81818;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 15.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  811 MW;  922879D5AB47687D CRC64;

  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      8 L 8


RESULT   5
AL16_CARMA
ID   AL16_CARMA     STANDARD;      PRT;     8 AA.
AC   P81819;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 16.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
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CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  813 MW;  7C286B45AB476878 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       8 L 8


RESULT   6
AL17_CARMA
ID   AL17_CARMA     STANDARD;      PRT;     8 AA.
AC   P81820;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 17.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       8       8       AMIDATION (POTENTIAL).
SQ   SEQUENCE   8 AA;  858 MW;  C82879D5AB46D865 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       8 L 8


RESULT   7
AL18_CARMA
ID   AL18_CARMA     STANDARD;      PRT;     8 AA.
AC   P81821;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 18.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       8       8       AMIDATION (POTENTIAL).
SQ   SEQUENCE   8 AA;  919 MW;  C82879D5AB569AB5 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       8 L 8


RESULT   8
ALL1_CYDPO
ID   ALL1_CYDPO     STANDARD;      PRT;     8 AA.
AC   P82152;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CYDIASTATIN 1.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  934 MW;  C82879C45B51F775 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       8 L 8


RESULT   9
ALL3_CYDPO
ID   ALL3_CYDPO     STANDARD;      PRT;     8 AA.
AC   P82154;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CYDIASTATIN 3.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
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```
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  926 MW;  C82879D5AB477415 CRC64;


  Query Match           36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      8 L 8


RESULT  10
ALL4_CALVO
ID   ALL4_CALVO     STANDARD;      PRT;     8 AA.
AC   P41840;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CALLATOSTATIN 4 (LEU-CALLATOSTATIN 4).
OS   Calliphora vomitoria (Blue blowfly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Oestroidea; Calliphoridae; Calliphora.
OX   NCBI_TaxID=27454;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Thoracic ganglion;
RX   MEDLINE=93211980; PubMed=8460157;
RA   Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA   Thorpe A.;
RT   "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria
RT   with sequence homology to cockroach allatostatins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN   [2]
RP   CHARACTERIZATION.
RX   MEDLINE=94291167; PubMed=8020069;
RA   Duve H., Thorpe A.;
RT   "Distribution and functional significance of Leu-callatostatins in
RT   the blowfly Calliphora vomitoria.";
RL   Cell Tissue Res. 276:367-379(1994).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
CC       A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
CC       INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
CC       BEHAVE AS POTENT INHIBITORS OF PERISTALIC MOVEMENTS. MAY ALSO
CC       FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC   -!- TISSUE SPECIFICITY: BRAIN, SUBOESOPHAGEAL GANGLION, RETROCEREBRAL
CC       COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY
CC       SYSTEM AND INTESTINE.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR   PIR; D47393; D47393.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8      8       AMIDATION.
FT   UNSURE        1      1       OR N.
SQ   SEQUENCE   8 AA;  954 MW;  D32879D5AB47740A CRC64;


  Query Match           36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      8 L 8


RESULT  11
ALL4_CYDPO
ID   ALL4_CYDPO     STANDARD;      PRT;     8 AA.
AC   P82155;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CYDIASTATIN 4.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  910 MW;  922879D5AB47740D CRC64;


  Query Match           36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      8 L 8


RESULT  12
ALL5_CYDPO
ID   ALL5_CYDPO     STANDARD;      PRT;     8 AA.
AC   P82156;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CYDIASTATIN 5.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  898 MW;  922879CABB58640D CRC64;


  Query Match           36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      8 L 8


RESULT  13
ALL6_CYDPO
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ID   ALL6_CYDPO     STANDARD;      PRT;     8 AA.
AC   P82157;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CYDIASTATIN 6.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  936 MW;  0B2879C45B573767 CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       1 L 1


RESULT  14
ALL7_CARMA
ID   ALL7_CARMA     STANDARD;      PRT;     8 AA.
AC   P81809; P81810; P81804;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   CARCINUSTATIN 7 [CONTAINS: CARCINUSTATIN 6; CARCINUSTATIN 1].
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   CHAIN         1       8       CARCINUSTATIN 7.
FT   CHAIN         2       8       CARCINUSTATIN 6.
FT   CHAIN         4       8       CARCINUSTATIN 1.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  825 MW;  922879CDCB4775BD CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       8 L 8


RESULT  15
ALL8_CARMA
ID   ALL8_CARMA     STANDARD;      PRT;     8 AA.
AC   P81811;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 8.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  795 MW;  922879CDCB47687D CRC64;


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       8 L 8


Search completed: December 13, 2001, 12:01:34
Job time: 297 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 12:01:16 ; Search time 34.38 Seconds
(without alignments)
34.037 Million cell updates/sec

Title: US-09-424-080A-2
Perfect score: 11
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 287

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	36.4	8	2	Q56429	Q56429 thermus aqu
2	4	36.4	8	2	P72279	P72279 rhodococcus
3	4	36.4	8	2	Q45889	Q45889 clostridium
4	4	36.4	8	2	O85406	O85406 coxiella bu
5	4	36.4	8	2	O87471	O87471 haemophilus
6	4	36.4	8	2	P77556	P77556 escherichia
7	4	36.4	8	2	Q51594	Q51594 escherichia
8	4	36.4	8	2	Q9ZIE9	Q9zie9 neisseria m
9	4	36.4	8	2	Q9ZEZ9	Q9zez9 buchnera ap
10	4	36.4	8	2	Q9X3K1	Q9x3k1 prochloroco
11	4	36.4	8	2	Q9RQ57	Q9rq57 buchnera ap
12	4	36.4	8	2	Q9RQ49	Q9rq49 buchnera ap
13	4	36.4	8	2	Q9R9C2	Q9r9c2 borrelia bu
14	4	36.4	8	2	Q9R5R2	Q9r5r2 shigella dy
15	4	36.4	8	2	Q9R4M3	Q9r4m3 enterococcu
16	4	36.4	8	2	Q9AGP4	Q9agp4 arthrobacte
17	4	36.4	8	3	P87225	P87225 saccharomyc
18	4	36.4	8	3	O13591	O13591 saccharomyc
19	4	36.4	8	3	Q9URB9	Q9urb9 saccharomyc
20	4	36.4	8	3	P82858	P82858 puccinia re
21	4	36.4	8	3	Q9HDS4	Q9hds4 aspergillus
22	4	36.4	8	4	Q15889	Q15889 homo sapien
23	4	36.4	8	4	Q15893	Q15893 homo sapien
24	4	36.4	8	4	Q15894	Q15894 homo sapien
25	4	36.4	8	4	Q15895	Q15895 homo sapien
26	4	36.4	8	4	Q15901	Q15901 homo sapien
27	4	36.4	8	4	Q16468	Q16468 homo sapien
28	4	36.4	8	4	Q9Y4J4	Q9y4j4 homo sapien
29	4	36.4	8	4	Q9Y4J3	Q9y4j3 homo sapien
30	4	36.4	8	4	O60773	O60773 homo sapien
31	4	36.4	8	4	Q9UMH9	Q9umh9 homo sapien
32	4	36.4	8	4	Q9UMC7	Q9umc7 homo sapien
33	4	36.4	8	4	Q9UHK1	Q9uhk1 homo sapien
34	4	36.4	8	4	Q9P0K3	Q9p0k3 homo sapien
35	4	36.4	8	4	Q9H4D3	Q9h4d3 homo sapien
36	4	36.4	8	4	Q9BYY5	Q9byy5 homo sapien
37	4	36.4	8	5	O15899	O15899 babesia ovi
38	4	36.4	8	5	O15896	O15896 babesia bov
39	4	36.4	8	5	P82618	P82618 periplaneta
40	4	36.4	8	6	O18854	O18854 canis famil
41	4	36.4	8	6	O02831	O02831 oryctolagus
42	4	36.4	8	6	Q9XSY1	Q9xsy1 canis famil
43	4	36.4	8	6	Q9TT78	Q9tt78 canis famil
44	4	36.4	8	6	Q9TRX8	Q9trx8 bos taurus
45	4	36.4	8	13	Q9PS69	Q9ps69 gallus gall

ALIGNMENTS

RESULT 1
Q56429
ID Q56429 PRELIMINARY; PRT; 8 AA.
AC Q56429;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE GAPDH (FRAGMENT).
OS Thermus aquaticus (subsp. thermophilus).
OC Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB-8;
RX MEDLINE=89025722; PubMed=3052437;
RA Bowen D., Littlechild J.A., Fothergill J.E., Watson H.C., Hall L.;
RT "Nucleotide sequence of the phosphoglycerate kinase gene from the
RT extreme thermophile Thermus thermophilus. Comparison of the deduced
RT amino acid sequence with that of the mesophilic yeast phosphoglycerate
RT kinase.";
RL Biochem. J. 254:509-517(1988).
DR EMBL; X12464; CAA31005.1; -.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 885 MW; 33C873333732C72B CRC64;

Query Match 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 L 1
|
Db 2 L 2

RESULT 2
P72279
ID P72279 PRELIMINARY; PRT; 8 AA.
AC P72279;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

```
DE   BIPHENYL DIOXYGENASE (FRAGMENT).
GN   BPHB.
OS   Rhodococcus globerulus.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OX   NCBI_TaxID=33008;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95255652; PubMed=7737502;
RA   Asturias J.A., Diaz E., Timmis K.N.;
RT   "The evolutionary relationship of biphenyl dioxygenase from gram-
RT   positive Rhodococcus globerulus P6 to multicomponent dioxygenases from
RT   gram-negative bacteria.";
RL   Gene 156:11-18(1995).
DR   EMBL; X80041; CAA56350.1; -.
KW   Dioxygenase.
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  989 MW;  EBD2CB1AB6D73406 CRC64;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      3 L 3


RESULT   3
Q45889
ID   Q45889      PRELIMINARY;      PRT;     8 AA.
AC   Q45889;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   HA-11 PROTEIN (FRAGMENT).
GN   HA-II.
OS   Clostridium botulinum.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1491;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=667AB;
RX   MEDLINE=96210012; PubMed=8631890;
RA   Hutson R.A., Zhou Y., Collins M.D., Johnson E.A., Hatheway C.L.,
RA   Sugiyama H.;
RT   "Genetic characterization of Clostridium botulinum type A containing
RT   silent type B neurotoxin gene sequences.";
RL   J. Biol. Chem. 271:10786-10792(1996).
DR   EMBL; X87850; CAA61130.1; -.
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  982 MW;  FE29D1B40B02D5B6 CRC64;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      8 L 8


RESULT   4
O85406
ID   O85406      PRELIMINARY;      PRT;     8 AA.
AC   O85406;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
OS   Coxiella burnetii.
OC   Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
OC   Coxiella group; Coxiella.
OX   NCBI_TaxID=777;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NINE MILE PHASE I;
RA   Willems H., Jaeger C., Baljer G.;
RT   "Physical and genetic map of the obligate intracellular bacterium
RT   Coxiella burnetii.";
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF064963; AAD09947.1; -.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   8 AA;  993 MW;  046B5AA453772727 CRC64;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      1 L 1


RESULT   5
O87471
ID   O87471      PRELIMINARY;      PRT;     8 AA.
AC   O87471;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   HIFA (FRAGMENT).
GN   HIFA.
OS   Haemophilus influenzae.
OC   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC   Haemophilus.
OX   NCBI_TaxID=727;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=EAGAN (E1A);
RX   MEDLINE=98389689; PubMed=9721313;
RA   Mhlanga-Mutangadura T., Morlin G., Smith A.L., Eisenstark A.,
RA   Golomb M.;
RT   "Evolution of the major pilus gene cluster of Haemophilus
RT   influenzae.";
RL   J. Bacteriol. 180:4693-4703(1998).
DR   EMBL; AF071762; AAC35830.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   8 AA;  876 MW;  DAB44451A7272325 CRC64;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      3 L 3


RESULT   6
P77556
ID   P77556      PRELIMINARY;      PRT;     8 AA.
AC   P77556;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE   TRAY (FRAGMENT).
GN   TRAY.
OS   Escherichia coli.
OG   Plasmid IncFII R1.
```

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OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ECOR11;
RX   MEDLINE=96400908; PubMed=8807284;
RA   Boyd E.F., Hill C.W., Rich S.M., Hartl D.L.;
RT   "Mosaic structure of plasmids from natural populations of Escherichia
RT   coli.";
RL   Genetics 143:1091-1100(1996).
DR   EMBL; U50661; AAC44245.1; -.
DR   EMBL; U50650; AAC44234.1; -.
DR   EMBL; U50651; AAC44235.1; -.
DR   EMBL; U50652; AAC44236.1; -.
DR   EMBL; U50653; AAC44237.1; -.
DR   EMBL; U50654; AAC44238.1; -.
DR   EMBL; U50655; AAC44239.1; -.
DR   EMBL; U50656; AAC44240.1; -.
DR   EMBL; U50657; AAC44241.1; -.
DR   EMBL; U50658; AAC44242.1; -.
DR   EMBL; U50659; AAC44243.1; -.
DR   EMBL; U50660; AAC44244.1; -.
KW   Plasmid.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  834 MW;  D335A5B0544735A1 CRC64;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
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Qy       1 L 1
           |
Db       3 L 3


RESULT   7
Q51594
ID   Q51594      PRELIMINARY;      PRT;     8 AA.
AC   Q51594;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   COPB PROTEIN (FRAGMENT).
OS   Escherichia coli.
OG   Plasmid IncFI ColV2-K94.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86223772; PubMed=2423502;
RA   Weber P.C., Palchaudhuri S.;
RT   "Incompatibility repressor in a RepA-like replicon of the IncFI
RT   plasmid ColV2-K94.";
RL   J. Bacteriol. 166:1106-1112(1986).
DR   EMBL; M13472; AAA23194.1; -.
KW   Plasmid.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  998 MW;  0F37205AA73416D7 CRC64;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       1 L 1


RESULT   8
Q9ZIE9
ID   Q9ZIE9      PRELIMINARY;      PRT;     8 AA.
AC   Q9ZIE9;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   CARBAMOYL-PHOSPHATE SYNTHASE SUBUNIT B (FRAGMENT).
GN   CARB.
OS   Neisseria meningitidis.
OC   Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX   NCBI_TaxID=487;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1527;
RX   MEDLINE=95291461; PubMed=7773412;
RA   Lawson F.S., Billowes F.M., Dillon J.A.;
RT   "Organization of carbamoyl-phosphate synthase genes in Neisseria
RT   gonorrhoeae includes a large, variable intergenic sequence which is
RT   also present in other Neisseria species.";
RL   Microbiology 141:0-0(0).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1527;
RA   Brinkman F.S.L., Francis F.M., Dillon J.R.;
RT   "Complexity of the variable sequence between the carbamoyl-phosphate
RT   synthase genes of Neisseria species.";
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF029361; AAC78449.1; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  988 MW;  FA372AB1B4032766 CRC64;


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  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       7 L 7


RESULT   9
Q9ZEZ9
ID   Q9ZEZ9      PRELIMINARY;      PRT;     8 AA.
AC   Q9ZEZ9;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.12) (FRAGMENT).
GN   LEUA.
OS   Buchnera aphidicola.
OG   Plasmid pBRc1.
OC   Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX   NCBI_TaxID=9;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99028904; PubMed=9812361;
RA   Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
RT   "Structure and evolution of the leucine plasmids carried by the
RT   endosymbiont (Buchnera aphidicola) from aphids of the family
RT   Aphididae.";
RL   FEMS Microbiol. Lett. 168:43-49(1998).
DR   EMBL; AJ006874; CAA07290.1; -.
KW   Lyase; Plasmid.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  917 MW;  FE205042D6C5B446 CRC64;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
```

```
Db      8 L 8


RESULT  10
Q9X3K1
ID   Q9X3K1      PRELIMINARY;      PRT;     8 AA.
AC   Q9X3K1;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   CYTOCHROME B (FRAGMENT).
GN   PETB.
OS   Prochlorococcus sp.
OC   Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC   Prochlorococcus.
OX   NCBI_TaxID=1220;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Urbach E., Chisholm S.W.;
RT   "Genetic diversity in Prochlorococcus populations flow cytometrically
RT   sorted from the Sargasso Sea and Gulf Stream.";
RL   Limnol. Oceanog. 43:1615-1630(1998).
DR   EMBL; AF070193; AAD23233.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  799 MW;  10376865B72866D3 CRC64;

  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      4 L 4


RESULT  11
Q9RQ57
ID   Q9RQ57      PRELIMINARY;      PRT;     8 AA.
AC   Q9RQ57;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   NIFS PROTEIN HOMOLOG (FRAGMENT).
GN   NIFS.
OS   Buchnera aphidicola.
OC   Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX   NCBI_TaxID=9;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20022990; PubMed=10555290;
RA   Clark M.A., Moran N.A., Baumann P.;
RT   "Sequence evolution in bacterial endosymbionts having extreme base
RT   compositions.";
RL   Mol. Biol. Evol. 16:1586-1598(1999).
DR   EMBL; AF130812; AAF13797.1; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  980 MW;  F3A73B504771A336 CRC64;

  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 L 7


RESULT  12
Q9RQ49
ID   Q9RQ49      PRELIMINARY;      PRT;     8 AA.
AC   Q9RQ49;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   NIFS PROTEIN HOMOLOG (FRAGMENT).
GN   NIFS.
OS   Buchnera aphidicola.
OC   Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX   NCBI_TaxID=9;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20022990; PubMed=10555290;
RA   Clark M.A., Moran N.A., Baumann P.;
RT   "Sequence evolution in bacterial endosymbionts having extreme base
RT   compositions.";
RL   Mol. Biol. Evol. 16:1586-1598(1999).
DR   EMBL; AF130814; AAF13805.1; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  992 MW;  F3A73B5047672336 CRC64;

  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      3 L 3


RESULT  13
Q9R9C2
ID   Q9R9C2      PRELIMINARY;      PRT;     8 AA.
AC   Q9R9C2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   PLASMID CP32-3, POSSIBLE PARTITION PROTEINS, COMPLETE CDS (FRAGMENT).
OS   Borrelia burgdorferi (Lyme disease spirochete).
OG   Plasmid cp32-3.
OC   Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX   NCBI_TaxID=139;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B31;
RX   MEDLINE=98361033; PubMed=9695920;
RA   Stevenson B., Casjens S., Rosa P.;
RT   "Evidence of past recombination events among the genes encoding the
RT   Erp antigens of Borrelia burgdorferi.";
RL   Microbiology 144:0-0(0).
DR   EMBL; AF022480; AAC35445.1; -.
KW   Plasmid.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  985 MW;  E8B41B41A735B446 CRC64;

  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      4 L 4


RESULT  14
Q9R5R2
ID   Q9R5R2      PRELIMINARY;      PRT;     8 AA.
AC   Q9R5R2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   31,000 DA PRODUCT OF ORFB.
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```
OS   Shigella dysenteriae.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Shigella.
OX   NCBI_TaxID=622;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92085268; PubMed=1660923;
RA   Polard P., Prere M.F., Chandler M., Fayet O.;
RT   "Programmed translational frameshifting and initiation at an AUU codon
RT   in gene expression of bacterial insertion sequence IS911.";
RL   J. Mol. Biol. 222:465-477(1991).
SQ   SEQUENCE   8 AA;  902 MW;  FE2DCAFB586AE336 CRC64;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       8 L 8


RESULT  15
Q9R4M3
ID   Q9R4M3      PRELIMINARY;      PRT;     8 AA.
AC   Q9R4M3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   COB1=BACTERIAL SEX PHEROMONE.
OS   Enterococcus faecalis (Streptococcus faecalis).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC   Enterococcus.
OX   NCBI_TaxID=1351;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95290767; PubMed=7772836;
RA   Nakayama J., Abe Y., Ono Y., Isogai A., Suzuki A.;
RT   "Isolation and structure of the Enterococcus faecalis sex pheromone,
RT   cOB1, that induces conjugal transfer of the hemolysin/bacteriocin
RT   plasmids, pOB1 and pYI1.";
RL   Biosci. Biotechnol. Biochem. 59:703-705(1995).
SQ   SEQUENCE   8 AA;  741 MW;  83D87732C732CDC2 CRC64;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       4 L 4


Search completed: December 13, 2001, 12:01:16
Job time: 304 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 11:57:18 ; Search time 36.87 Seconds
(without alignments)
16.072 Million cell updates/sec

Title: US-09-424-080A-2
Perfect score: 11
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 15187

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	36.4	8	2	AAP10369	Peptide secretin d
2	4	36.4	8	2	AAP10585	GH, gastric and pa
3	4	36.4	8	2	AAP10461	Antibiotic octapep
4	4	36.4	8	2	AAP10462	Antibiotic octapep
5	4	36.4	8	2	AAP10463	Antibiotic octapep
6	4	36.4	8	2	AAP10464	Antibiotic octapep
7	4	36.4	8	3	AAP20291	Bombesin analog pe
8	4	36.4	8	3	AAP20292	Bombesin analog pe
9	4	36.4	8	3	AAP20293	Bombesin analog pe
10	4	36.4	8	3	AAP20294	Bombesin analog pe
11	4	36.4	8	3	AAP20254	Opioid peptide 2.
12	4	36.4	8	3	AAP20374	Cargutocin. Synth
13	4	36.4	8	3	AAP20141	Protected insulin
14	4	36.4	8	3	AAP20381	Protected insulin
15	4	36.4	8	3	AAP20382	Protected insulin
16	4	36.4	8	3	AAP20303	Gastrointestinal m
17	4	36.4	8	3	AAP20483	De-amino-6-carba-o
18	4	36.4	8	3	AAP20485	Novel antibiotic n
19	4	36.4	8	3	AAP20162	Ppetide antibiotic
20	4	36.4	8	4	AAP30571	Analgesic enkephal
21	4	36.4	8	4	AAP30572	Analgesic enkephal
22	4	36.4	8	4	AAP30573	Analgesic enkephal
23	4	36.4	8	4	AAP30574	Analgesic enkephal
24	4	36.4	8	4	AAP30575	Analgesic enkephal
25	4	36.4	8	4	AAP30448	Substrate for coll
26	4	36.4	8	5	AAP40472	Cyclic renin inhib
27	4	36.4	8	5	AAP40473	Cyclic renin inhib
28	4	36.4	8	5	AAP40474	Cyclic renin inhib
29	4	36.4	8	5	AAP40485	Sequence of peptid
30	4	36.4	8	5	AAP40101	Sequence at antige
31	4	36.4	8	5	AAP40682	Sequence at antige
32	4	36.4	8	5	AAP40288	Sequence of interm
33	4	36.4	8	5	AAP40492	Sequence of renin
34	4	36.4	8	5	AAP40497	Sequence of renin
35	4	36.4	8	5	AAP40578	Sequence of peptid
36	4	36.4	8	5	AAP40579	Sequence of peptid
37	4	36.4	8	5	AAP40572	Sequence of cyclic
38	4	36.4	8	5	AAP40573	Sequence of cyclic
39	4	36.4	8	5	AAP40574	Sequence of cyclic
40	4	36.4	8	5	AAP40575	Sequence of cyclic
41	4	36.4	8	5	AAP40412	Luliberin analogue
42	4	36.4	8	5	AAP40415	Opioid peptide pre
43	4	36.4	8	5	AAP40299	Proenkephalin, the
44	4	36.4	8	6	AAP50009	Sequence of an AA
45	4	36.4	8	22	AAB61602	Somatostatin agoni

ALIGNMENTS

RESULT 1
AAP10369
ID AAP10369 standard; Protein; 8 AA.
XX
AC AAP10369;
XX
DT 16-DEC-1992 (first entry)
XX
DE Peptide secretin derivative #8.
XX
KW secretin; insulin; diabetes; pancreas; islets of langerhans; glucose.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 6
FT /label= OTHER
FT /note= "pyroglutamic acid"
FT Misc-difference 8
FT /label= OTHER
FT /note= "-OR3 or -NR1R2
FT where R1 and R2 are H, C1-C6 alkyl,
FT C3-C8 cycloalkyl. R1 and R2 may also be
FT linked together to form a cyclic gp having
FT at least 1 hetero atom ie the amide bonded N,
FT opt. contg. an additional hetero atom eg. N,
FT O, or S.
FT where R3 is H, C1-C6 alkyl, C3-C8 cycloalkyl,
FT benzyl, phenacyl, phthalimidomethyl,
FT beta-methylthioethyl, 4-picolyl, and benzyl
FT substituted with nitro, methoxy, methyl,
FT halogen."
XX
PN US4265884-A.

```
XX
PD   05-MAY-1981.
XX
PF   24-SEP-1979;   79US-0078425.
XX
PR   05-SEP-1979;   79DK-0003710.
PR   28-SEP-1978;   78DK-0004304.
XX
PA   (NORI ) NORDISK INSULINLAB.
XX
PI   Kofod H;
XX
DR   WPI; 1981-38054D/21  (38054D).
XX
PT   Secretin related poly:peptide(s) - which potentiate glucose
PT   stimulated secretion of insulin
XX
PS   Claim 2; Column 6; 4pp; English.
XX
CC   This peptide is a derivative of the intestinal hormone secretin.
CC   They potentiate the glucose stimulated secretion of insulin from
CC   Langerhans' islets. They may be used to treat diabetics who have
CC   themselves lost the ability to liberate insulin from the Langerhans
CC   islets.
XX
SQ   Sequence   8 AA;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      5 l 5


RESULT   2
AAP10585
ID   AAP10585 standard; Protein; 8 AA.
XX
AC   AAP10585;
XX
DT   23-DEC-1992  (first entry)
XX
DE   GH, gastric and pancreatic secretion inhibitor (1).
XX
KW   Growth hormone; diabetes; acromegaly.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "D-form residue"
FT   Misc-difference 4
FT                   /note= "D-form residue"
FT   Misc-difference 8
FT                   /label= LEU, OTHER
FT                   /note= "LEU-ol"
FT   Disulfide-bond  2..7
XX
PN   EP29579-A.
XX
PD   03-JUN-1981.
XX
PF   13-JUN-1988;   88EP-0057316.
XX
PR   13-JUN-1980;   80CH-0004574.
PR   27-NOV-1979;   79CH-0010524.
XX
PA   (SANO ) SANDOZ AG.
XX
PI   Bauer W,  Pless J;
XX
DR   WPI; 1981-42362D/24  (42362D).
XX
PT   Polypeptide(s) contg. cysteine-terminal hexa:peptide fragment -
PT   useful as growth-hormone, gastric and pancreatic secretion
PT   inhibitors
XX
PS   Claim 4; Page 31; 35pp; English.
XX
CC   The peptide inhibits growth hormone secretion and can be used to
CC   treat diabetes, angiopathy and acromegaly.  It also inhibits gastric
CC   and pancreatic secretion and can be used to treat gastrointestinal
CC   disorders.
XX
SQ   Sequence   8 AA;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      8 l 8


RESULT   3
AAP10461
ID   AAP10461 standard; peptide; 8 AA.
XX
AC   AAP10461;
XX
DT   17-DEC-1992  (first entry)
XX
DE   Antibiotic octapeptin 1.
XX
KW   Staphylococcus aureus; Streptococcus pyogenes; Bacillus subtilis;
KW   Salmonella typhimurium; Shigella sonnei Ohara.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "D-Ser acetylated with beta-hydroxy-
FT                          anteisoundecanoic acid; forms a peptide
FT                          bond with Leu at position 8"
FT   Modified-site   2
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Modified-site   3
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Modified-site   6
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Modified-site   7
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Misc-difference 8
FT                   /note= "Forms peptide bond with Dab at position 1"
XX
PN   JP56087596-A.
XX
PD   16-JUL-1981.
XX
PF   18-DEC-1979;   79JP-0165150.
XX
PR   18-DEC-1979;   79JP-0165150.
XX
PA   (SHIO ) SHIONOGI KK.
XX
DR   WPI; 1981-63474D/35  (63474D).
XX
```

```
PT   Antibiotic octa:peptin D - prepd. by cultivating Bacillus gp. no.
PT   JP-301
XX
PS   Claim 2; Page 1; 6pp; Japanese.
XX
CC   The sequences given in AAP10461-4 are antibiotic octapeptins which
CC   have antimicrobial activity.  They are active against Staphylococcus
CC   aureus FDA209P, Streptococcus pyogenes C-203, Bacillus subtilis PCI
CC   219, Salmonella typhimurium and Shigella sonnei Ohara.
XX
SQ   Sequence   8 AA;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       4 l 4


RESULT   4
AAP10462
ID   AAP10462 standard; Protein; 8 AA.
XX
AC   AAP10462;
XX
DT   17-DEC-1992  (first entry)
XX
DE   Antibiotic octapeptin 2.
XX
KW   Staphylococcus aureus; Streptococcus pyogenes; Bacillus subtilis;
KW   Salmonella typhimurium; Shigella sonnei Ohara.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "D-Ser acetylated with beta-hydroxy-
FT                          isodecanoic acid; forms a peptide
FT                          bond with Leu at position 8"
FT   Modified-site   2
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Modified-site   3
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Modified-site   6
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Modified-site   7
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Misc-difference 8
FT                   /note= "Forms peptide bond with Dab at position 1"
XX
PN   JP56087596-A.
XX
PD   16-JUL-1981.
XX
PF   18-DEC-1979;   79JP-0165150.
XX
PR   18-DEC-1979;   79JP-0165150.
XX
PA   (SHIO ) SHIONOGI KK.
XX
DR   WPI; 1981-63474D/35  (63474D).
XX
PT   Antibiotic octa:peptin D - prepd. by cultivating Bacillus gp. no.
PT   JP-301
XX
PS   Claim 3; Page 1; 6pp; Japanese.
XX
CC   The sequences given in AAP10461-4 are antibiotic octapeptins which
CC   have antimicrobial activity.  They are active against Staphylococcus
CC   aureus FDA209P, Streptococcus pyogenes C-203, Bacillus subtilis PCI
CC   219, Salmonella typhimurium and Shigella sonnei Ohara.
XX
SQ   Sequence   8 AA;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       4 l 4


RESULT   5
AAP10463
ID   AAP10463 standard; Protein; 8 AA.
XX
AC   AAP10463;
XX
DT   17-DEC-1992  (first entry)
XX
DE   Antibiotic octapeptin 3.
XX
KW   Staphylococcus aureus; Streptococcus pyogenes; Bacillus subtilis;
KW   Salmonella typhimurium; Shigella sonnei Ohara.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "D-Ser acetylated with beta-hydroxy-
FT                          decanoic acid; forms a peptide
FT                          bond with Leu at position 8"
FT   Modified-site   2
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Modified-site   3
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Modified-site   6
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Modified-site   7
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Misc-difference 8
FT                   /note= "Forms peptide bond with Dab at position 1"
XX
PN   JP56087596-A.
XX
PD   16-JUL-1981.
XX
PF   18-DEC-1979;   79JP-0165150.
XX
PR   18-DEC-1979;   79JP-0165150.
XX
PA   (SHIO ) SHIONOGI KK.
XX
DR   WPI; 1981-63474D/35  (63474D).
XX
PT   Antibiotic octa:peptin D - prepd. by cultivating Bacillus gp. no.
PT   JP-301
XX
PS   Claim 4; Page 1; 6pp; Japanese.
XX
CC   The sequences given in AAP10461-4 are antibiotic octapeptins which
CC   have antimicrobial activity.  They are active against Staphylococcus
CC   aureus FDA209P, Streptococcus pyogenes C-203, Bacillus subtilis PCI
```

```
CC   219, Salmonella typhimurium and Shigella sonnei Ohara.
XX
SQ   Sequence   8 AA;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       4 l 4


RESULT   6
AAP10464
ID   AAP10464 standard; Protein; 8 AA.
XX
AC   AAP10464;
XX
DT   17-DEC-1992  (first entry)
XX
DE   Antibiotic octapeptin 4.
XX
KW   Staphylococcus aureus; Streptococcus pyogenes; Bacillus subtilis;
KW   Salmonella typhimurium; Shigella sonnei Ohara.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "D-Ser acetylated with beta-hydroxy-
FT                          isoundecanoic acid; forms a peptide
FT                          bond with Leu at position 8"
FT   Modified-site   2
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Modified-site   3
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Modified-site   6
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Modified-site   7
FT                   /label= OTHER
FT                   /note= "alpha, gamma-diaminobutyric acid"
FT   Misc-difference 8
FT                   /note= "Forms peptide bond with Dab at position 1"
XX
PN   JP56087596-A.
XX
PD   16-JUL-1981.
XX
PF   18-DEC-1979;   79JP-0165150.
XX
PR   18-DEC-1979;   79JP-0165150.
XX
PA   (SHIO ) SHIONOGI KK.
XX
DR   WPI; 1981-63474D/35  (63474D).
XX
PT   Antibiotic octa:peptin D - prepd. by cultivating Bacillus gp. no.
PT   JP-301
XX
PS   Claim 5; Page 2; 6pp; Japanese.
XX
CC   The sequences given in AAP10461-4 are antibiotic octapeptins which
CC   have antimicrobial activity.  They are active against Staphylococcus
CC   aureus FDA209P, Streptococcus pyogenes C-203, Bacillus subtilis PCI
CC   219, Salmonella typhimurium and Shigella sonnei Ohara.
XX
SQ   Sequence   8 AA;


  Query Match             36.4%;  Score 4;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       4 l 4


RESULT   7
AAP20291
ID   AAP20291 standard; peptide; 8 AA.
XX
AC   AAP20291;
XX
DT   09-DEC-1992  (first entry)
XX
DE   Bombesin analog peptide.
XX
KW   Bombesin; hypothermic; analgesic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /label= Gly, Ala, D-Ala, Asn, D-Asn, Gln, D-Gln,
FT                           His, D-His, Leu, D-Leu, Met, D-Met, Phe,
FT                           D-Phe, Thr, D-Thr, Val or D-Val
FT   Misc-difference 5
FT                   /label= D-Ala or Gly
XX
PN   US4331661-A.
XX
PD   25-MAY-1982.
XX
PF   03-OCT-1980;   80US-0193621.
XX
PR   03-OCT-1980;   80US-0193621.
XX
PA   (SALK-) SALK INST BIOLOGICA.
XX
PI   Marki WE,  Brown MR,  Rivier JEF;
XX
DR   WPI; 1982-48049E/23  (48049E).
XX
PT   Octa:peptide bombesin analogues - having hypothermic and
PT   analgesic props.
XX
PS   Claim 1; Column 6; 5pp; English.
XX
CC   The peptide may be preceded by a formyl, acetyl, propionyl, acrylyl
CC   or benzoyl group at its C-terminal.  The peptide may be used for
CC   reducing the body temp. of a mammal, as well as for inducing
CC   analgesia.  It produces hypothermia when injected i.c., but not
CC   when given i.v. or s.c.  See also AAP20292-94.
XX
SQ   Sequence   8 AA;


  Query Match             36.4%;  Score 4;  DB 3;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       7 l 7


RESULT   8
AAP20292
ID   AAP20292 standard; peptide; 8 AA.
XX
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```
AC   AAP20292;
XX
DT   09-DEC-1992  (first entry)
XX
DE   Bombesin analog peptide.
XX
KW   Bombesin; hypothermic; analgesic.
XX
OS   Synthetic.
XX
PN   US4331661-A.
XX
PD   25-MAY-1982.
XX
PF   03-OCT-1980;   80US-0193621.
XX
PR   03-OCT-1980;   80US-0193621.
XX
PA   (SALK-) SALK INST BIOLOGICA.
XX
PI   Marki WE,  Brown MR,  Rivier JEF;
XX
DR   WPI; 1982-48049E/23  (48049E).
XX
PT   Octa:peptide bombesin analogues - having hypothermic and
PT   analgesic props.
XX
PS   Claim 4; Column 7; 5pp; English.
XX
CC   The peptide may be preceded by a formyl, acetyl, propionyl, acrylyl
CC   or benzoyl group at its C-terminal.  The peptide may be used for
CC   reducing the body temp. of a mammal, as well as for inducing
CC   analgesia.  It produces hypothermia when injected i.c., but not
CC   when given i.v. or s.c.  See also AAP20291, AAP20293-4.
XX
SQ   Sequence   8 AA;


  Query Match             36.4%;  Score 4;  DB 3;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 l 7


RESULT   9
AAP20293
ID   AAP20293 standard; peptide; 8 AA.
XX
AC   AAP20293;
XX
DT   09-DEC-1992  (first entry)
XX
DE   Bombesin analog peptide.
XX
KW   Bombesin; hypothermic; analgesic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 5
FT                   /label= D-Ala
XX
PN   US4331661-A.
XX
PD   25-MAY-1982.
XX
PF   03-OCT-1980;   80US-0193621.
XX
PR   03-OCT-1980;   80US-0193621.
XX
PA   (SALK-) SALK INST BIOLOGICA.
XX
PI   Marki WE,  Brown MR,  Rivier JEF;
XX
DR   WPI; 1982-48049E/23  (48049E).
XX
PT   Octa:peptide bombesin analogues - having hypothermic and
PT   analgesic props.
XX
PS   Claim 6; Column 7; 5pp; English.
XX
CC   The peptide may be preceded by a formyl, acetyl, propionyl, acrylyl
CC   or benzoyl group at its C-terminal.  The peptide may be used for
CC   reducing the body temp. of a mammal, as well as for inducing
CC   analgesia.  It produces hypothermia when injected i.c., but not
CC   when given i.v. or s.c.  See also AAP20291-2, AAP20294.
XX
SQ   Sequence   8 AA;


  Query Match             36.4%;  Score 4;  DB 3;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 l 7


RESULT  10
AAP20294
ID   AAP20294 standard; peptide; 8 AA.
XX
AC   AAP20294;
XX
DT   09-DEC-1992  (first entry)
XX
DE   Bombesin analog peptide.
XX
KW   Bombesin; hypothermic; analgesic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /label= D-Glu
FT   Misc-difference 5
FT                   /label= D-Ala
XX
PN   US4331661-A.
XX
PD   25-MAY-1982.
XX
PF   03-OCT-1980;   80US-0193621.
XX
PR   03-OCT-1980;   80US-0193621.
XX
PA   (SALK-) SALK INST BIOLOGICA.
XX
PI   Marki WE,  Brown MR,  Rivier JEF;
XX
DR   WPI; 1982-48049E/23  (48049E).
XX
PT   Octa:peptide bombesin analogues - having hypothermic and
PT   analgesic props.
XX
PS   Claim 8; Column 8; 5pp; English.
XX
CC   The peptide may be preceded by a formyl, acetyl, propionyl, acrylyl
CC   or benzoyl group at its C-terminal.  The peptide may be used for
CC   reducing the body temp. of a mammal, as well as for inducing
CC   analgesia.  It produces hypothermia when injected i.c., but not
CC   when given i.v. or s.c.  See also AAP20291-3.
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```
XX
SQ   Sequence   8 AA;

  Query Match             36.4%;  Score 4;  DB 3;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 l 7


RESULT  11
AAP20254
ID   AAP20254 standard; Protein; 8 AA.
XX
AC   AAP20254;
XX
DT   27-NOV-1992  (first entry)
XX
DE   Opioid peptide 2.
XX
KW   Hypothalamus; acetic acid; chromatography.
XX
OS   Sus scrofa.
XX
PN   JP57134451-A.
XX
PD   19-AUG-1982.
XX
PF   13-FEB-1981;   81JP-0020707.
XX
PR   13-FEB-1981;   81JP-0020707.
XX
PA   (SUNC ) SUN CHEMICAL CORP.
XX
DR   WPI; 1982-82141E/39  (82141E).
XX
PT   Opiate peptide cpds. - useful as morphine-like analgesics
XX
PS   Claim 1; Page 2; 6pp; Japanese.
XX
CC   The sequences given in AAP20253-4 are opioid peptides.  They can be
CC   used as morphine-like analgesics.  They can be obtained by
CC   extraction of porcine hypothalamus with acetic acid, followed by
CC   chromatography with "Sephadex" and by HPLC with "Bondapak C-18".
XX
SQ   Sequence   8 AA;

  Query Match             36.4%;  Score 4;  DB 3;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      5 l 5


RESULT  12
AAP20374
ID   AAP20374 standard; Protein; 8 AA.
XX
AC   AAP20374;
XX
DT   18-JAN-1993  (second entry)
XX
DE   Cargutocin.
XX
KW   Oxytocic agent; linear molecule; cyclization.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   5
FT                   /label= OTHER
FT                   /note= "L-aminosuberic acid"
FT   Modified-site   1
FT                   /note= "The amino gp of Tyr1 is condensed to the
FT                   side chain of Asu5."
FT   Modified-site   5
FT                   /note= "The amino gp of Tyr1 is condensed to the
FT                   side chain of Asu5."
XX
PN   JP57062245-A.
PN   JP57062246-A.
XX
PD   15-APR-1982.
XX
PF   01-OCT-1980;   80JP-0137970.
XX
PR   01-OCT-1980;   80JP-0137970.
XX
PA   (YOSH ) YOSHITOMI PHARM IND KK.
XX
DR   WPI; 1982-42246E/21  (42246E).
XX
PT   Cargutocin prepn. from l-amino suberic acid ester - by successive
PT   prolongation of peptide chain followed by its cyclisation and
PT   reaction with hydrazine
XX
PS   Disclosure; Page 1; 4pp; Japanese.
XX
CC   The sequence given is cargutocin which is produced by reacting a
CC   precursor molecule (see also AAP20373) with a linear peptide
CC   H-Gly-Leu-Gly-NH2 to produce the product molecule.  Cargutocin is
CC   useful as an oxytocic agent.  The product provides high solubility
CC   of reactants in solvents and high yield in cyclization.
XX
SQ   Sequence   8 AA;

  Query Match             36.4%;  Score 4;  DB 3;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      7 l 7


RESULT  13
AAP20141
ID   AAP20141 standard; peptide; 8 AA.
XX
AC   AAP20141;
XX
DT   27-NOV-1992  (first entry)
XX
DE   Protected insulin B-chain (1).
XX
KW   Hydrazide; DNP; 2,4-dinitrophenyl; DPM; diphenylmethyl.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "Nalpha-protected, removable by mild acid
FT                   hydrolysis"
FT   Modified-site   5
FT                   /note= "DNP-protected or His-H"
FT   Duplication     7
FT                   /note= "DPM-protected"
FT   Modified-site   8
FT                   /note= "alkylated (sic) or amidated"
```

```
XX
PN   DD155321-A.
XX
PD   02-JUN-1982.
XX
PF   08-AUG-1980;   80DD-0223203.
XX
PR   15-DEC-1980;   80DD-0226078.
XX
PA   (AROL/) AROLD H.
XX
PI   Arold H,  Mueller A,  Schwuchow C;
XX
DR   WPI; 1982-83706E/40  (83706E).
XX
PT   Prepn. of protected insulin B-chain octa:peptide - using
PT   di:nitro-phenyl gp. for histidine protection
XX
PS   Claim 1; Page 10; 11pp; German.
XX
CC   The cpd. is useful as intermediate for synthesis of insulin or its
CC   B chain.  The DNP gp. provides temporary protection for the His side
CC   chain and is readily removed by hydrazinolysis, e.g. during
CC   conversion of the cpd. to the hydrazide.
XX
SQ   Sequence   8 AA;


  Query Match             36.4%;  Score 4;  DB 3;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      6 l 6


RESULT  14
AAP20381
ID   AAP20381 standard; Protein; 8 AA.
XX
AC   AAP20381;
XX
DT   27-NOV-1992  (first entry)
XX
DE   Protected insulin B-chain (2).
XX
KW   DNP; 2,4-dinitrophenyl; DPM; diphenylmethyl.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "Boc-protected"
FT   Modified-site   5
FT                   /note= "DNP-protected"
FT   Modified-site     7
FT                   /note= "DPM-protected"
FT   Modified-site   8
FT                   /note= "Gly-OMe"
XX
PN   DD155321-A.
XX
PD   02-JUN-1982.
XX
PF   08-AUG-1980;   80DD-0223203.
XX
PR   15-DEC-1980;   80DD-0226078.
XX
PA   (AROL/) AROLD H.
XX
PI   Arold H,  Mueller A,  Schwuchow C;
XX
DR   WPI; 1982-83706E/40  (83706E).
XX
PT   Prepn. of protected insulin B-chain octa:peptide - using
PT   di:nitro-phenyl gp. for histidine protection
XX
PS   Example 8; Page 8; 11pp; German.
XX
CC   The cpd. is useful as intermediate for synthesis of insulin or its
CC   B chain.
XX
SQ   Sequence   8 AA;


  Query Match             36.4%;  Score 4;  DB 3;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      6 l 6


RESULT  15
AAP20382
ID   AAP20382 standard; Protein; 8 AA.
XX
AC   AAP20382;
XX
DT   27-NOV-1992  (first entry)
XX
DE   Protected insulin B-chain (3).
XX
KW   DNP; 2,4-dinitrophenyl; DPM; diphenylmethyl.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "Boc-protected"
FT   Duplication     7
FT                   /note= "DPM-protected"
FT   Modified-site   8
FT                   /note= "amidated"
XX
PN   DD155321-A.
XX
PD   02-JUN-1982.
XX
PF   08-AUG-1980;   80DD-0223203.
XX
PR   15-DEC-1980;   80DD-0226078.
XX
PA   (AROL/) AROLD H.
XX
PI   Arold H,  Mueller A,  Schwuchow C;
XX
DR   WPI; 1982-83706E/40  (83706E).
XX
PT   Prepn. of protected insulin B-chain octa:peptide - using
PT   di:nitro-phenyl gp. for histidine protection
XX
PS   Example 9; Page 9; 11pp; German.
XX
CC   The cpd. is useful as intermediate for synthesis of insulin or its
CC   B chain.
XX
SQ   Sequence   8 AA;


  Query Match             36.4%;  Score 4;  DB 3;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

Qy 1 L 1
|
Db 6 1 6

Search completed: December 13, 2001, 11:57:18
Job time: 101 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: December 13, 2001, 11:56:05 ; Search time 20.43 Seconds
(without alignments)
8.812 Million cell updates/sec

Title: US-09-424-080A-2
Perfect score: 11
Sequence: 1 LXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 8027

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	36.4	8	1	US-07-234-381A-1	Sequence 1, Appli
2	4	36.4	8	1	US-07-643-948A-1	Sequence 1, Appli
3	4	36.4	8	1	US-07-643-948A-3	Sequence 3, Appli
4	4	36.4	8	1	US-07-620-410-3	Sequence 3, Appli
5	4	36.4	8	1	US-07-780-081-1	Sequence 1, Appli
6	4	36.4	8	1	US-07-717-316B-4	Sequence 4, Appli
7	4	36.4	8	1	US-07-737-852-3	Sequence 3, Appli
8	4	36.4	8	1	US-07-621-670-6	Sequence 6, Appli
9	4	36.4	8	1	US-07-657-769B-10	Sequence 10, Appl
10	4	36.4	8	1	US-07-657-769B-40	Sequence 40, Appl
11	4	36.4	8	1	US-07-657-769B-50	Sequence 50, Appl
12	4	36.4	8	1	US-07-876-280-11	Sequence 11, Appl
13	4	36.4	8	1	US-07-729-513-3	Sequence 3, Appli
14	4	36.4	8	1	US-07-718-274A-16	Sequence 16, Appl
15	4	36.4	8	1	US-07-718-274A-49	Sequence 49, Appl
16	4	36.4	8	1	US-07-792-259-6	Sequence 6, Appli
17	4	36.4	8	1	US-07-830-330-4	Sequence 4, Appli
18	4	36.4	8	1	US-07-725-331-58	Sequence 58, Appl
19	4	36.4	8	1	US-07-626-589-12	Sequence 12, Appl
20	4	36.4	8	1	US-07-752-101A-4	Sequence 4, Appli
21	4	36.4	8	1	US-07-946-237-5	Sequence 5, Appli
22	4	36.4	8	1	US-07-946-237-6	Sequence 6, Appli
23	4	36.4	8	1	US-07-932-200-17	Sequence 17, Appl
24	4	36.4	8	1	US-07-820-154A-36	Sequence 36, Appl
25	4	36.4	8	1	US-07-920-519-9	Sequence 9, Appli
26	4	36.4	8	1	US-07-920-519-11	Sequence 11, Appl
27	4	36.4	8	1	US-08-057-184-11	Sequence 11, Appl
28	4	36.4	8	1	US-08-057-184-12	Sequence 12, Appl
29	4	36.4	8	1	US-07-872-644-25	Sequence 25, Appl
30	4	36.4	8	1	US-08-086-410-6	Sequence 6, Appli
31	4	36.4	8	1	US-08-086-410-8	Sequence 8, Appli
32	4	36.4	8	1	US-07-791-213D-70	Sequence 70, Appl
33	4	36.4	8	1	US-08-149-106-16	Sequence 16, Appl
34	4	36.4	8	1	US-08-149-106-49	Sequence 49, Appl
35	4	36.4	8	1	US-07-603-675-6	Sequence 6, Appli
36	4	36.4	8	1	US-07-908-317-4	Sequence 4, Appli
37	4	36.4	8	1	US-07-841-997A-7	Sequence 7, Appli
38	4	36.4	8	1	US-08-103-490A-6	Sequence 6, Appli
39	4	36.4	8	1	US-08-030-731A-12	Sequence 12, Appl
40	4	36.4	8	1	US-08-030-731A-23	Sequence 23, Appl
41	4	36.4	8	1	US-07-968-781A-33	Sequence 33, Appl
42	4	36.4	8	1	US-07-968-781A-55	Sequence 55, Appl
43	4	36.4	8	1	US-07-968-781A-57	Sequence 57, Appl
44	4	36.4	8	1	US-07-968-781A-61	Sequence 61, Appl
45	4	36.4	8	5	PCT-US94-05150-5	Sequence 5, Appli

ALIGNMENTS

```
RESULT 1
US-07-234-381A-1
; Sequence 1, Application US/07234381A
; Patent No. 5185147
; GENERAL INFORMATION:
;   APPLICANT: Papsidero, Lawrence D
;   TITLE OF INVENTION: Short Polypeptide Sequences Useful In The Production
;   TITLE OF INVENTION: And Detection Of Antibodies Against Human Immunodeficiency
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Elman & Wilf
;     STREET: 20 West Third Street
;     STREET: P.O. Box 703
;     CITY: Media
;     STATE: PA
;     COUNTRY: USA
;     ZIP: 19063
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy Disk
;     COMPUTER: IBM PC-compatible
;     OPERATING SYSTEM: MS-DOS
;     SOFTWARE: WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/07/234,381A
;     FILING DATE: 19880819
;     CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Elman, Gerry J.
;     REGISTRATION NUMBER: 24,404
;     REFERENCE/DOCKET NUMBER: C8-038
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 215 892 9580
;     TELEFAX: 215 892 9577
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 8 amino acids
;     TYPE: AMINO ACID
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-07-234-381A-1

  Query Match          36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
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Db       2 L 2
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RESULT   2
US-07-643-948A-1
; Sequence 1, Application US/07643948A
; Patent No. 5200505
;  GENERAL INFORMATION:
;    APPLICANT:  Kazutoh TAKESAKO et al.
;    TITLE OF INVENTION:  No. 5200505el R106 Compounds
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 Kb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  DisplayWrite
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/643,948A
;      FILING DATE:  19910122
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek Jr.
;      REGISTRATION NUMBER:  33,367
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:  202-371-8856
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    ORIGINAL SOURCE:
;      ORGANISM:  Aureobasidium
;    FEATURE:
;      NAME/KEY:  modified-site
;      LOCATION:  1
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  /note= "MeVal"
;    FEATURE:
;      NAME/KEY:  modified-site
;      LOCATION:  3
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  /note=
;      OTHER INFORMATION:  "N-methylphenylalanine, B-hydroxy-N-methylphenylalanine or
;      OTHER INFORMATION:  Phe"
;    FEATURE:
;      NAME/KEY:  modified-site
;      LOCATION:  5
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  /note= "aIle, Val or Leu"
;    FEATURE:
;      NAME/KEY:  modified-site
;      LOCATION:  6
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  /note= "MeVal or Val"
;    FEATURE:
;      NAME/KEY:  modified-site
;      LOCATION:  8
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  /note= "B-hydroxy-N-
;      OTHER INFORMATION:  methylvaline, gamma-hydroxy-N-methylvaline, MeVal, Val,
;      OTHER INFORMATION:  N,B-dimethylaspartic acid, B-hydroxy-N-methylphenylalanine,
;      OTHER INFORMATION:  or N-methylphenylalanine."
;    FEATURE:
;      NAME/KEY:  modified-site
;      LOCATION:  8
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  /note= "N-methyl-2,3-
;      OTHER INFORMATION:  didehydrovaline or N-methyl-3,4-didehydrovaline."
;    FEATURE:
;      NAME/KEY:  modified-site
;      LOCATION:  8
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  /note= "wherein the amino
;      OTHER INFORMATION:  acid has a substituent 2-hydroxy-3-methylbutanoic acid or
;      OTHER INFORMATION:  2-hydroxy-3-methylpentanoic acid bound to location 1."
US-07-643-948A-1


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
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Db       7 L 7


RESULT   3
US-07-643-948A-3
; Sequence 3, Application US/07643948A
; Patent No. 5200505
;  GENERAL INFORMATION:
;    APPLICANT:  Kazutoh TAKESAKO et al.
;    TITLE OF INVENTION:  No. 5200505el R106 Compounds
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 Kb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  DisplayWrite
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/643,948A
;      FILING DATE:  19910122
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek Jr.
;      REGISTRATION NUMBER:  33,367
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:  202-371-8856
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    ORIGINAL SOURCE:
;      ORGANISM:  Aureobasidium
;    FEATURE:
;      NAME/KEY:  modified-site
;      LOCATION:  1
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  /note= "MeVal"
;    FEATURE:
;      NAME/KEY:  modified-site
;      LOCATION:  3
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  /note=
;      OTHER INFORMATION:  "N-methylphenylalanine, Sarcosine, N-methylserine or
;      OTHER INFORMATION:  B-oxo-N-methylphenylalanine"
;    FEATURE:
;      NAME/KEY:  modified-site
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;       LOCATION:  5
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:  /note= "aIle"
;     FEATURE:
;       NAME/KEY:  modified-site
;       LOCATION:  6
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:  /note= "MeVal"
;     FEATURE:
;       NAME/KEY:  modified-site
;       LOCATION:  8
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:  /note= "B-hydroxy-N-
;       OTHER INFORMATION:  methylvaline or Sarcosine, wherein the amino acid has a
;       OTHER INFORMATION:  substituent 2-hydroxy-3-methylpentanoic acid which is bound
;       OTHER INFORMATION:  to the amino acid in location 1 to form the cyclic peptide."
;     FEATURE:
;       NAME/KEY:
;       LOCATION:
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:  /note= "Excluding wherein
;       OTHER INFORMATION:  location 3 is N-methylphenylalanine and location 8 is
;       OTHER INFORMATION:  B-hydroxy-N-methylvaline."
US-07-643-948A-3


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       7 L 7


RESULT   4
US-07-620-410-3
; Sequence 3, Application US/07620410
; Patent No. 5217953
;  GENERAL INFORMATION:
;    APPLICANT:  Gozes, Illana
;    APPLICANT:  Brenneman, Douglas E.
;    APPLICANT:  Fridkin, Mati
;    APPLICANT:  Moody, Terry
;    TITLE OF INVENTION:  A NOVEL VASOACTIVE INTESTINAL PEPTIDE
;    TITLE OF INVENTION:  ANTAGONIST
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CUSHMAN, DARBY & CUSHMAN
;      STREET:  1615 L. Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/620,410
;      FILING DATE:  19901130
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Scott, Watson T.
;      REGISTRATION NUMBER:  26,581
;      REFERENCE/DOCKET NUMBER:  WTS/5683/82679
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3000
;      TELEFAX:  (202) 822-0944
;      TELEX:  248453 CUSH
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-620-410-3


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       1 L 1


RESULT   5
US-07-780-081-1
; Sequence 1, Application US/07780081
; Patent No. 5229366
;  GENERAL INFORMATION:
;    APPLICANT:  TSUKADA, Yoshihisa
;    APPLICANT:  ORIKASA, Atsushi
;    TITLE OF INVENTION:  PEPTIDE-CONTAINING POLYETHYLENE GLYCOL
;    TITLE OF INVENTION:  DERIVATIVES AND APPLICATION THEREOF
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sughrue, Mion, Zinn, Macpeak and Seas
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/780,081
;      FILING DATE:  19911021
;      CLASSIFICATION:  530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-293-7060
;      TELEFAX:  202-293-7860
;      TELEX:  6491103
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-780-081-1


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       3 L 3


RESULT   6
US-07-717-316B-4
; Sequence 4, Application US/07717316B
; Patent No. 5229495
;  GENERAL INFORMATION:
;    APPLICANT:  Ichijo, Hidenori; Miyazono, Kohei;
;    APPLICANT:  R nnstrand, Lars; Hellman, Uls; Wernstedt, Christer;
;    APPLICANT:  Heldin, Carl-Henrik
;    TITLE OF INVENTION:  Substantially Pure Receptor-Like
```

```
;    TITLE OF INVENTION:  TGF-a1 Binding Molecules And Uses Thereof
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/717,316B
;      FILING DATE:  19910618
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5229495man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 259
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-717-316B-4


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       6 L 6


RESULT   7
US-07-737-852-3
; Sequence 3, Application US/07737852
; Patent No. 5243027
;  GENERAL INFORMATION:
;    APPLICANT:  Mimura, Tsutomu
;    APPLICANT:  Kohama, Yasuhiro
;    APPLICANT:  Nagata, Kazuhiko
;    APPLICANT:  Tsurutani, Ryoichi
;    TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME
;    TITLE OF INVENTION:  INHIBITOR
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sughrue, Mion, Zinn, Macpeak & Seas
;      STREET:  2100 Pennsylvania Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/737,852
;      FILING DATE:  19910731
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 02-46975
;      FILING DATE:  26-FEB-1990
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)293-7060
;      TELEFAX:  (202)293-7860
;      TELEX:  6491103
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Bacillus stearothermophilus
;      STRAIN:  NCA-1503
US-07-737-852-3


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
           |
Db       8 L 8


RESULT   8
US-07-621-670-6
; Sequence 6, Application US/07621670
; Patent No. 5254801
;  GENERAL INFORMATION:
;    APPLICANT:  Dotson, Stanton B.
;    TITLE OF INVENTION:  Heterologous Dominant Conditional Lethal
;    TITLE OF INVENTION:  Genes and Use Thereof
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis R. Hoerner, Jr. Monsanto Co. BB4F
;      STREET:  700 Chesterfield Village Parkway
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/621,670
;      FILING DATE:  19901203
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hoerner Jr., Dennis R.
;      REGISTRATION NUMBER:  30,914
;      REFERENCE/DOCKET NUMBER:  38-21(10523)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6099
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-621-670-6


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 L 1
```

```
Db      3 L 3


RESULT   9
US-07-657-769B-10
; Sequence 10, Application US/07657769B
; Patent No. 5256766
;  GENERAL INFORMATION:
;    APPLICANT:  COUGHLIN, SHAUN R.
;    TITLE OF INVENTION:  RECOMBINANT RECEPTOR AND RELATED
;    TITLE OF INVENTION:  PHARMACEUTICALS
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IRELL & MANELLA
;      STREET:  545 MIDDLEFIELD ROAD, SUITE 200
;      CITY:  MENLO PARK
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/657,769B
;      FILING DATE:  19910219
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2000-0502.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-657-769B-10


  Query Match             36.4%;  Score 4;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 L 1
          |
Db      3 L 3


RESULT  10
US-07-657-769B-40
; Sequence 40, Application US/07657769B
; Patent No. 5256766
;  GENERAL INFORMATION:
;    APPLICANT:  COUGHLIN, SHAUN R.
;    TITLE OF INVENTION:  RECOMBINANT RECEPTOR AND RELATED
;    TITLE OF INVENTION:  PHARMACEUTICALS
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IRELL & MANELLA
;      STREET:  545 MIDDLEFIELD ROAD, SUITE 200
;      CITY:  MENLO PARK
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/657,769B
;      FILING DATE:  19910219
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2000-0502.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-657-769B-40


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Db      1 L 1


RESULT  11
US-07-657-769B-50
; Sequence 50, Application US/07657769B
; Patent No. 5256766
;  GENERAL INFORMATION:
;    APPLICANT:  COUGHLIN, SHAUN R.
;    TITLE OF INVENTION:  RECOMBINANT RECEPTOR AND RELATED
;    TITLE OF INVENTION:  PHARMACEUTICALS
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IRELL & MANELLA
;      STREET:  545 MIDDLEFIELD ROAD, SUITE 200
;      CITY:  MENLO PARK
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/657,769B
;      FILING DATE:  19910219
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2000-0502.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
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;      TELEX:  706141
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-657-769B-50
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  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
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Db       3 L 3


RESULT  12
US-07-876-280-11
; Sequence 11, Application US/07876280
; Patent No. 5262158
;  GENERAL INFORMATION:
;    APPLICANT:  Payne, Jewel M.
;    APPLICANT:  Cannon, Raymond J.C.
;    APPLICANT:  Bagley, Angela L.
;    TITLE OF INVENTION:  No. 5262158el Bacillus thuringiensis Isolates for
;    TITLE OF INVENTION:  Controlling Acarides
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David R. Saliwanchik
;      STREET:  2421 N.W. 41st Street, Suite A-1
;      CITY:  Gainesville
;      STATE:  FL
;      COUNTRY:  USA
;      ZIP:  32606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/876,280
;      FILING DATE:  19920430
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Saliwanchik, David R.
;      REGISTRATION NUMBER:  31,794
;      REFERENCE/DOCKET NUMBER:  M/S 104
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  904-375-8100
;      TELEFAX:  904-372-5800
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-876-280-11


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Qy       1 L 1
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Db       7 L 7


RESULT  13
US-07-729-513-3
; Sequence 3, Application US/07729513
; Patent No. 5270175
;  GENERAL INFORMATION:
;    APPLICANT:  Moll, Benjamin A.
;    TITLE OF INVENTION:  Methods and Compositions for Producing
;    TITLE OF INVENTION:  Metabolic Products from Algae
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James M. Heslin
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  96301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/729,513
;      FILING DATE:  19910712
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heslin, James M.
;      REGISTRATION NUMBER:  29,541
;      REFERENCE/DOCKET NUMBER:  12176-21/A0118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-729-513-3


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Db       7 L 7


RESULT  14
US-07-718-274A-16
; Sequence 16, Application US/07718274A
; Patent No. 5284756
;  GENERAL INFORMATION:
;    APPLICANT:  Grinna, Lynn
;    APPLICANT:  Parsons, Thomas F.
;    APPLICANT:  Theofan, Georgia
;    TITLE OF INVENTION:  Osteogenic Factor
;    NUMBER OF SEQUENCES:  63
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/718,274A
;      FILING DATE:  19910620
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/415,555
;      FILING DATE:  04-OCT-1989
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/256,034
;      FILING DATE:  11-OCT-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharp, Jeffrey S.
;      REGISTRATION NUMBER:  31,879
;      REFERENCE/DOCKET NUMBER:  27129/9430
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-718-274A-16


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Qy      1 L 1
          |
Db      1 L 1


RESULT  15
US-07-718-274A-49
; Sequence 49, Application US/07718274A
; Patent No. 5284756
;  GENERAL INFORMATION:
;    APPLICANT:  Grinna, Lynn
;    APPLICANT:  Parsons, Thomas F.
;    APPLICANT:  Theofan, Georgia
;    TITLE OF INVENTION:  Osteogenic Factor
;    NUMBER OF SEQUENCES:  63
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/718,274A
;      FILING DATE:  19910620
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/415,555
;      FILING DATE:  04-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/256,034
;      FILING DATE:  11-OCT-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharp, Jeffrey S.
;      REGISTRATION NUMBER:  31,879
;      REFERENCE/DOCKET NUMBER:  27129/9430
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
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;      TYPE:  AMINO ACID
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;    MOLECULE TYPE:  protein
US-07-718-274A-49


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  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      8 L 8


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USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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STRUCTURE FILE UPDATES:   11 DEC 2001  HIGHEST RN 374745-93-4
DICTIONARY FILE UPDATES:  11 DEC 2001  HIGHEST RN 374745-93-4

TSCA INFORMATION NOW CURRENT THROUGH July 7, 2001

  Please note that search-term pricing does apply when
  conducting SmartSELECT searches.

Crossover limits have been increased.  See HELP CROSSOVER for details.

Calculated physical property data is now available.  See HELP PROPERTIES
for more information.  See STNote 27, Searching Properties in the CAS
Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

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                NS][YH][SRDNA][PRDL]/SQSP
L3            2 SEA FILE=REGISTRY ABB=ON  PLU=ON  L2 AND  8/SQL
L4            2 SEA FILE=REGISTRY ABB=ON  PLU=ON  (L1 OR L3)


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     FILE 'HCAPLUS' ENTERED AT 12:31:17 ON 13 DEC 2001
L7            1 S L4

     FILE 'REGISTRY' ENTERED AT 12:31:37 ON 13 DEC 2001

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     arginyl- (9CI)  (CA INDEX NAME)
FS   PROTEIN SEQUENCE; STEREOSEARCH
SQL  8

SEQ      1 LRRRRHRR
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MF   C48 H92 N28 O9
SR   CA
LC   STN Files:   CA, CAPLUS, TOXCENTER, TOXLIT

Absolute stereochemistry.
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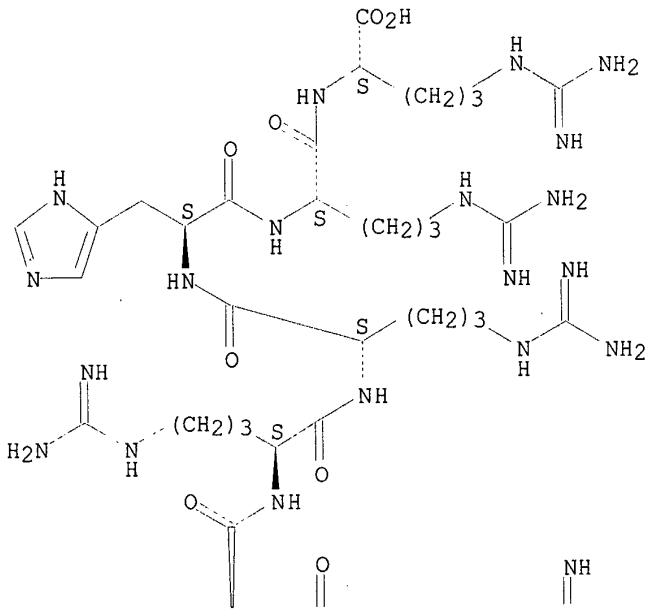
Point of Contact:
Jan Delaval
Librarian-Physical Sciences
CM1 1E01 Tel: 308-4498

PAGE 1-A



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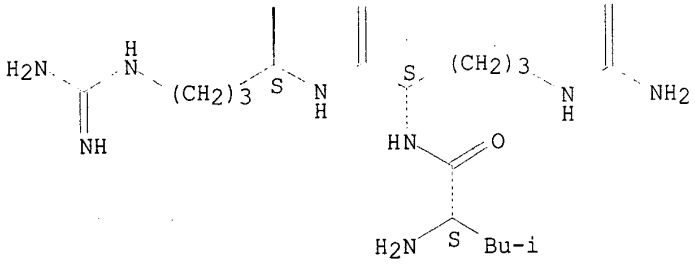

1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 130:33014

L4 ANSWER 2 OF 2 REGISTRY COPYRIGHT 2001 ACS
RN 216579-39-4 REGISTRY
CN L-Proline, L-leucyl-L-threonyl-L-.alpha.-glutamyl-L-lysyl-L-lysyl-L-tyrosyl-L-seryl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
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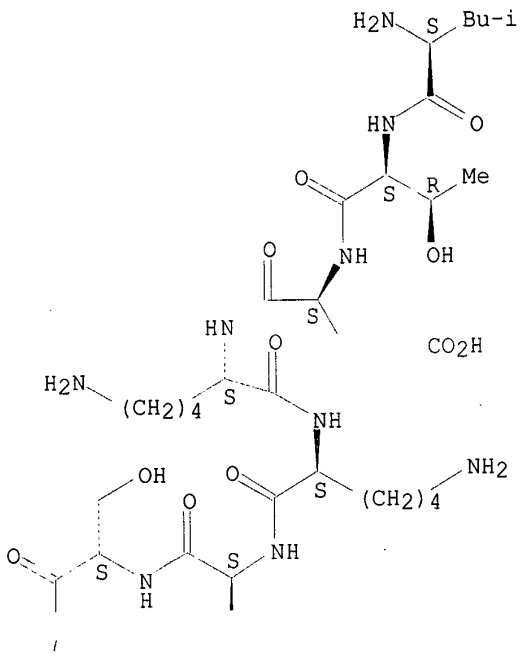
Absolute stereochemistry.

PAGE 1-A



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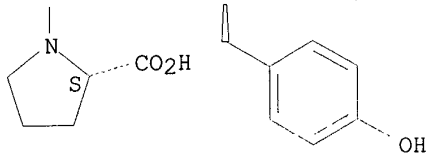

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1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 130:33014

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USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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FILE COVERS 1947 - 13 Dec 2001 VOL 135 ISS 25
FILE LAST UPDATED: 11 Dec 2001 (20011211/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

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HCAplus now provides online access to patents and literature covered in CA from 1947 to the present. On April 22, 2001, bibliographic information and abstracts were added for over 2.2 million references published in CA from 1947 to 1966.

=> d all l7

L7 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:789037 HCAPLUS
DN 130:33014
TI Compositions for enhancing immunosuppressants pharmaceutical activities
IN Zavialov, Vladimir Petrovich; Vasilenko, Raisa Nikolaevna; Dolgikh, Dmitry Aleksandrovich; Kirpichnikov, Mikhail Petrovich; Navolotskaya, Elena Vitalievna; Korpela, Timo Kalevi
PA Russia
SO PCT Int. Appl., 26 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM A61K038-04
ICS A61K038-13; A61K038-21
CC 1-7 (Pharmacology)
Section cross-reference(s): 15
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9852594	A1	19981126	WO 1998-FI418	19980518
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	FI 9702121	A	19981120	FI 1997-2121	19970519
	AU 9874352	A1	19981211	AU 1998-74352	19980518
	EP 981359	A1	20000301	EP 1998-921528	19980518
	R: AT, DE, ES, FR, GB, IT, SE, FI				
PRAI	FI 1997-2121		19970519		
	WO 1998-FI418		19980518		

AB The present invention provides compns. for efficient amplification of immunosuppressive activity of cyclosporins, FK506 or rapamycin to decrease therapeutical dose of immunosuppressants and, as a consequence, avoidance of their undesirable side effects during organ and tissue transplantation, and treatment of different diseases. These compns. include cyclosporins, FK506 or rapamycin and biol. active peptides corresponding to the high-affinity binding/anti-lymphoproliferative site of IFNs-a,b,w,t, or recombinant proteins having the amino acid sequences corresponding to the said site.
ST immunosuppressant adjuvant formulation peptide
IT Interferon .tau.
Interferon .alpha.
Interferon .beta.
RL: PRP (Properties)
(antilymphoproliferative site of; compns. for enhancing immunosuppressant pharmaceutical activities)
IT Adenocarcinoma inhibitors
Anti-inflammatory drugs
Antirheumatic drugs
Autoimmune diseases
Drug bioavailability
Immunosuppressants

Leukemia inhibitors
Lupus erythematosus
Lymphoma inhibitors
Myasthenia gravis
Psoriasis
Transplant (organ)
Uveitis
(compns. for enhancing immunosuppressant pharmaceutical activities)

IT Interferon .alpha.2
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)
(compns. for enhancing immunosuppressant pharmaceutical activities)

IT Peptides, biological studies
RL: PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(compns. for enhancing immunosuppressant pharmaceutical activities)

IT Interferons
RL: PRP (Properties)
(interferon .omega., antilymphoproliferative site of; compns. for enhancing immunosuppressant pharmaceutical activities)

IT Antitumor agents
(myeloma; compns. for enhancing immunosuppressant pharmaceutical activities)

IT **216579-39-4D**, analogs **216579-44-1D**, analogs
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)
(compns. for enhancing immunosuppressant pharmaceutical activities)

IT 53123-88-9, Rapamycin 79217-60-0D, Cyclosporin, derivs. 104987-11-3, Fk506
RL: PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(compns. for enhancing immunosuppressant pharmaceutical activities)

RE.CNT 5
RE
(1) University of Florida; WO 9009806 A2 1990 HCAPLUS
(2) University of Florida; WO 9410313 A2 1994 HCAPLUS
(3) Vacsyn, S; FR 2706772 A1 1994 HCAPLUS
(4) Zarogoulidis, K; Lung Cancer 1996, V15(2), P197 MEDLINE
(5) Zav'Yalov, V; Mol Immunol 1995, V32(6), P425 HCAPLUS

7/7/2 (Item 2 from file: 73)
DIALOG(R)File 73:EMBASE

06929781 EMBASE No: 1997214260
Structure-activity of type I interferons
Viscomi G.C.
G.C. Viscomi, Alfa Wassermann, Dept. of Biotechnology/Immunology, Via Ragazzi Del '99 N.5, 40133 Bologna Italy
Biotherapy (BIOTHERAPY (THE NETHERLANDS)) (Netherlands) 1997, 10/1 (59-86)
CODEN: BTHRE ISSN: 0921-299X
DOCUMENT TYPE: Journal; Review
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 126

Type I IFNs consitute a family of proteins exhibiting high **homology** in primary, secondary, and tertiary structures. They interact with the same receptor and transmit signals to cellular nucleus through a similar mechanism, eliciting roughly homogeneous biological activity. Nevertheless, the members of that family, IFNalpha species, IFNbeta and IFNomega, due to local differences in the structure sometime show distinct properties. From the reported data it results that even minute changes or differences in the primary sequences could be responsible for a significant variety of biological actions, thus inducing to the hypothesis that Type I IFNs, rather than to be the result of a redundant replication during the evolution, play definite roles in the defense of living organisms to foreign agents.

7/7/3 (Item 3 from file: 73)
DIALOG(R)File 73:EMBASE

06064616 EMBASE No: 1995095061
Human type I interferons: **Structure and function**
Kontsek P.
Institute of Virology, Slovak Academy of Sciences, Dubravska cesta 9,942 46 Bratislava Slovakia
Acta Virologica (ACTA VIROL.) (Czech Republic) 1994, 38/6 (345-360)
CODEN: AVIRA ISSN: 0001-723X
DOCUMENT TYPE: Journal; Review
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Human **type I interferons** (IFNs) comprise a family of 13 IFN-alpha subypes and single species of IFN-beta and IFN-omega. Their 20% overall sequence **homology** determines identical secondary and tertiary folding of polypeptides. Three-dimensional models suggest that the globular structure of type I IFNs consists of a bundle of 5 alpha-helices, which might form two polypeptide domains. Disulfide bond Cys 29-Cys 139 stabilizes both domains in a bioactive configuration. The IFN molecule exerts its functional entity only as an organic polypeptide complex and therefore molecular fragments apparently lack biological activity. IFN-beta, IFN-omega and some IFN-alpha subtypes are glycoproteins, but the sugar moiety was found to be neither structurally nor functionally relevant. Type I IFNs share a common cellular receptor, a fact that implies a high structural conservativity of their receptor-binding areas. Two conservative hydrophilic regions associated with the amino acids (aa) 30-41 and 120-145 appear to constitute the basic framework of receptor recognition site in type I IFNs. However, the individual IFN-(sub)types induce different spectra of biological effects which reflect some specificity in modelling of binding sites. Besides a subtle sequential heterogeneity in the segments aa 30-41 and 120-145, also the variable hydrophilic aa regions 23-26, 68-85 and 112-121 are responsible for structural and functional individuality among human type I IFNs. The interaction between IFN and its receptor seems to be a complex event which triggers simultaneously antiviral, antiproliferative and immunomodulating actions, although different parts of

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         2597795  I
          282134  INTERFERON?
            2791  TYPE(W)I(W)INTERFERON?
         2995840  REVIEW?
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...examined 50 records  (100)
...examined 50 records  (150)
...completed examining records
      S6     106  RD S5 (unique items)
?s s6 and homology
           106  S6
        237758  HOMOLOGY
      S7     3  S6 AND HOMOLOGY
?t s7/7/all
```

7/7/1 (Item 1 from file: 73)

DIALOG(R)File 73:EMBASE

10784174 EMBASE No: 2000265957

HIV-1 gp41 and type I interferon. **Sequence** homology **and biological as well as clinical implications**

Chen Y.-H.; Xiao Y.; Dierich M.P.

Prof. Y.-H. Chen, Laboratory of Immunology, Res. Centre Medical Research, Tsinghua University, Beijing 100084 China

Immunologic Research (IMMUNOL. RES.) (United States) 2000, 22/1 (61-66)

CODEN: IMRSE ISSN: 0257-277X

DOCUMENT TYPE: Journal; Review

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 38

HIV-1 gp41-like human **type I interferon** (IFN) could inhibit lymphocyte proliferation and up-modulate MHC class I and II and ICAM-1 molecule expression. Sequence comparison indicates that a similar epitope RILAV-YLKD exists between N-domain of gp41 and two regions in IFN-alpha (aa29-35 and 113-129), IFN-beta (aa31-37 and 125-138) and IFN-omega (aa29-35 and 123-136), which was shown to form IFN-alpha/beta-receptor binding site. Weak sequence similarity was also found to exist in both regions on gp41 and type I IFN of murine and bovine. Experimental studies indicated that a common immunological epitope exists between gp41 and IFN-alpha and -beta. Antibodies against human IFN-alpha and -beta recognized the common immunological epitope and inhibited gp41-binding to the potential cellular receptor protein p45. Moreover, the polyclonal antibody to IFN-beta completely inhibited gp41-binding to human T, B cells and monocytic cells, while IFN-alpha could only inhibit this binding incompletely. It was interestingly observed that human IFN-beta after preincubating with cells could incompletely inhibit the binding of gp41 to human B cells and monocytic cells, and very weakly inhibit the binding to human T cells, indicating that the receptor for IFN-beta-binding may be involved in gp41 binding. This potential relationship may be based on the amino acid sequence **homology** in the receptor binding region between gp41 and IFN-beta. It was observed that the increased levels of antibodies against human IFN-alpha and -beta exist in HIV-1-infected individuals and are associated with the common epitope on gp41. Besides, several studies provided experimental evidence that the common immunological epitope could induce protective activity against HIV-1. The IFN-alpha-based vaccine has showed a significant reduction of disease progression in IFN-alpha-vaccine-treated HIV-infected patients. Recent experimental evidence indicates that gp41 and IFN-beta were involved in downregulation of CCR5 expression and induction of cell activation or signal transduction. Whether it may be performed by a similar mechanism is still to be investigated.

IFN molecule are not involved equally in eliciting of respective basal activities.

?ds

Set	Items	Description
S1	0	(INTERFERON?AND ALBEFERON)
S2	0	(INTEFERON?) AND ALBEFERON?
S3	14	INTERFERON? AND ALBEFERON?
S4	9	RD S3 (unique items)
S5	152	TYPE(W)I(W)INTERFERON? AND REVIEW?
S6	106	RD S5 (unique items)
S7	3	S6 AND HOMOLOGY

?

that albebetin possesses the properties of the molten globule state. Grafting of the octapeptide to the N-terminus of this de novo protein affects its structure. We show here that **albeferon** maintains a secondary s content of albebetin; it becomes more compact and much more stable toward urea-induced unfolding as compared to albebetin and even possesses some weak tertiary structure (at least around Tyr!7). This means that the structure of the artificial protein albebetin can be improved by a simple procedure of octapeptide grafting to its N-terminus.

4/7/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11277016 BIOSIS NO.: 199800058348
Synthetic octapeptide alpha-peptoferon and de novo protein albeferon **have the same anti-proliferative activity as human** interferon **alpha2.**
AUTHOR: Zav'yalov V P(a); Vasilenko R N(a); Navolotskaya E V(a); Dolgikh D P(a); Kirpichnikov M P; Abramov V M(a)
AUTHOR ADDRESS: (a)Inst. Immunol. Eng., Lyubuchany**Russia
JOURNAL: Journal of Interferon and Cytokine Research 17 (SUPPL. 2):pS99 Oct., 1997
CONFERENCE/MEETING: Annual Meeting of the International Society for Interferon and Cytokine Research San Diego, California, USA October 19-24, 1997
SPONSOR: International Society for Interferon and Cytokine Research
ISSN: 1079-9907
RECORD TYPE: Citation
LANGUAGE: English

4/7/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

10921786 BIOSIS NO.: 199799542931
Interferons **alpha/beta and their receptors: Place in the hierarchy of cytokines.**
AUTHOR: Zav'yalov Vladimir P(a); Zav'yalova Galina A
AUTHOR ADDRESS: (a)Inst. Immunological Engineering, 142380 Lyubuchany, Moscow Region**Russia
JOURNAL: APMIS 105 (3):p161-186 1997
ISSN: 0903-4641
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: **Interferons** alpha/beta (IFNs-alpha/beta) are the first cytokines to be produced by recombinant DNA technology. They regulate growth and differentiation, affecting cellular communication, signal transduction pathways and immunological control. This review focuses on the relationships between the structure and biological activities of IFNs-alpha/beta induced as a result of specific interactions with different types of polypeptide receptors as well as on the role of glycolipids in the modulation of these activities. The discovery of the primary structure homology of HuIFNs-alpha and thymus hormone-thymosin alpha-1 (TM-alpha-1), the experimental finding of the competition between IFN-alpha and TM-alpha-1 for common receptors and the reproduction by reHuIFN-alpha-2 of TM-alpha-1 immunomodulating activities create the basis of reHuIFN-alpha therapeutics instead of TM-alpha-1 and potentiation of vaccines by reHuIFN-alpha. The first successful attempt at grafting of the HuIFN-alpha-2s TM-alpha-1-like immunomodulating site to the designed de novo protein **albeferon** is described. This article also aims at reviewing recent data concerning the structure of other cytokines and their receptors. Their reciprocal structure-function taxonomy is proposed. The place of IFNs-alpha/beta and their receptors in the hierarchy of cytokines is determined.

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